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GenCore version 5.1.6
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October 21, 2004, 06:36:06; Search time 40 Seconds (without alignments) 942.924 Million cell updates/sec US-10-628-395-2 1987 1 MDTIFLWSLLLLFFGSQASR......FIMKHNPTESILFWGRVTNP 392 283416 seqs, 96216763 residues OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	neuroserpin precur ZG-21p protein - r	l carc	rsor -	thrombin	lated	elastase	activa	proteinase inhibit	ibitor	activa	inhibit	inhibit		nexin	activa	activa	contrapsin precurs	elated	man	ne pro	[validat	Jap	d III 1	H		, III 1	nhibit	activa
ption	erpin prote	is cel	precu	cal th	nin-re		nogen	nase i	se inh		nase i	lase	pid - uic	erived	nogen	nogen	d uisd	pein-r	ը - ը	n seri		min -	rombin	rombin	proteina	rombir	nase i	nogen
Description	euros	squamous cell car	eupin-	lacen	ovalbumin-related	leukocyte	plasminogen	rotei	lasta	plasminogen	proteinase	proteinase	serpin	glia-d	plasminogen	plasminogen	contra	contrapsin-relat	bomapin - human	headpin serine	ovalbumin	ovalbumin	antithrombin	antithrombin	serine	antithrombin	proteinase inhibit	plasminogen
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	7.4.7	010	02	81		21	65	17	83	32	88	96	62	74	45	61	53	75	84	18		33	ღ	11	.07	64	73	ιΡΊ
<del>a</del>	S70647 S49162	138201	I38202	A48681	DYCH	A4242	JC426	148717	S273	A350	A57488	B27496	8389	A37274	S06745	A34761	JX0129	823675	I39184	JC7118	OACH	\$11433	XHHU3	159611	831507	JX0364	A59273	ITHUP
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Length	410	390	390	376	388	379	400	397	379	402	378	397	378	398	402	402	418	418	397	391	386	383	464	465	418	431	374	402
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Ū	788.5	650	635	589	586	577.5	577	575	573.5	570.5	569	562.5	561	558	558	555.5	553.5	552	548.5	547.5	547	544.5		m		535	m	ന
	1 7 7 6	ım	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

alpha-1-antichymot	antithrombin III p	intracellular coag	antithrombin III -	serine proteinase	plasminogen activa	alpha-1-antiprotei	alpha-1-antiprotei	alpha-1-antitrypsi	proteinase inhibit	serine proteinase	alpha-1-antiprotei	serine proteinase	kallikrein-binding	kallikrein-binding	protein C05E4.1 [i
ITHUC	828219	A55533	A61435	I50494	A32853	JX0154	JX0267	A54968	B59273	S11320	S54981	808102	S19724	B29131	D88940
Н	Н	7	7	0	7	~	0	7	7	N	0	0	N	~	Ŋ
433	465	408	433	410	415	413	413	413	376	408	413	403	417	416	359
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26.5	26.4	26.3	26.2	25.9	25.9	25.9	25.6	25.5	25.5	25.5	25.3	25.2	25.1	25.1	24.9
526.5 26.5	524 26.4	523.5 26.3	_	10						506 25.5				498 25.1	•

## ALIGNMENTS

ange 09-Jul-2004 B.; Sonderegger, P. inhibitor.	PIDN:CAA96493.1.	410; 7; Gaps 3;	GITLVLEMVQL 61   : :   : :   SIAIAMGMIEL 62	ALYLQEGFTVKE 121  :  :	EFGPLTRLVLVN 181 :              DFSALTHLVLIN 182	SSLNYQVL 237		ATSTGIHIPVI 357 	
#text_ch Kuhn, T. protease 70795	00; NID:g1359667; 72> ed <sig> ental <mat></mat></sig>	Length Indels	FLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKD-NIIFSPLGITLVLEMYQL 	GAKGKAQQQIRQTLXQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKE 	QYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGFLTRLVLVN ::   :: :::	AIYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVL 	ELSYKGDEFSLIIILPABGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVD  :  :         :: :    : : :    :	FKDVLXSLAITEIFSGGCDL.SGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVI 	VTNP 392
1) /ision 13-M /; Stoeckli / secreted	A, Residues: 1-410 <ost1> A,COSS-references: UNIPROT.Q90935; EMBL:Z71930; NID:G A,Experimental source: brain A,Accession: S77695 A,Molecule type: protein A,Residues: 17-40;243-257,288-293;309-317 <ost2> C,Superfamily: Serpin C,Keywords: serline proteinase inhibitor C,Keywords: serline proteinase inhibitor E,11-16/Domain: signal sequence #status predicted <sig>E;11-6/Domain: signal sequence #status experimental <am.< td=""><td>39.7%; Score 788.5; DB 2; 40.0%; Pred. No. 7.3e-45; ive 92; Mismatches 138;</td><td>RCSAQKNTEFAVDLN : :   :   :   :   KTNFPDETIAELSVNVY</td><td>QQETSAGEEFLVLKSF(       FDSLKNGEEFTFLKDL</td><td>LVDFQDAKACAEMISTV :   :      NIDFSQSAAVATHINK</td><td>BDTQLINFTKKNGSTVK:  : ::   : : : SNTRTFSFTKDDETEVQ:</td><td>PAEGMDIEEVEKLITA( : : :     :   SRQEVPLVTLEPLVKA</td><td>GGCDLSGITDSSEVYVV   : :: :  :  : RSADLTAMSDNKELYL</td><td>MSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP</td></am.<></sig></ost2></ost1>	39.7%; Score 788.5; DB 2; 40.0%; Pred. No. 7.3e-45; ive 92; Mismatches 138;	RCSAQKNTEFAVDLN : :   :   :   :   KTNFPDETIAELSVNVY	QQETSAGEEFLVLKSF(       FDSLKNGEEFTFLKDL	LVDFQDAKACAEMISTV :   :      NIDFSQSAAVATHINK	BDTQLINFTKKNGSTVK:  : ::   : : : SNTRTFSFTKDDETEVQ:	PAEGMDIEEVEKLITA( : : :     :   SRQEVPLVTLEPLVKA	GGCDLSGITDSSEVYVV   : :: :  :  : RSADLTAMSDNKELYL	MSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP
RESULT 1 S70647  neuroserpin precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 14-Feb-1997 #sequence_revision 13-N C;Accession: S70647; S77695 R;Oservander, T.; Concarteee, J.; Stoeckli R;MD J. 15, 2944-2953, 1996 A;Title: Neuroserpin, an axonally secreted A;Reference number: S70647; MUID:96272154; A;Molecule type: mRNA	A,Residues: 1-410 <0ST1> A,CCSs.references: UNIPROT:090935; A,RCSssion: S77695 A,Molccule type: protein A,Residues: 17-40;243-257;288-293;3C C,Superfamily: Serpin C,Keywords: serine proteinase inhibi F;1-140/Product: neuroserpin #statu	ch 1 Similarity 40. 158; Conservative							
RESULT 1 S70647 neuroserpin precursor - (C,Species: Gallus gallus (C,Date: 14-Feb-1997 #sequ C,Accession: S70647; S77,Ryoterwalder, T.; Conta R,Osterwalder, T.; Conta A,Title: Neuroserpin, an A,Reference number: S70647 A,Accession: S70647 A,Aolecule type: mRNA	A,Residues: 1.410 <0STI A,COSS-references: UNA A,Experimental source: A,Accession: S77695 A,Molecule (vpe: protei A,Residues: 17-40,243-2 C,Superfamily: Serpin C,Reywords: serine prot F,1-16/Domain: signal 8 F,1-16/Domain: signal 8	Query Match Best Local Similarity Matches 158; Conser	Oy 5 Db 3	Oy 62 Db 63	Oy 122 Db 123	Oy 182 Db 183	Oy 238 Db 243	Oy 298 Db 303	Qy 358
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; PID:gl3

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AjAccessum: 2020.
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NyAlternate names: proteinase inhibitor 11 (PI11); squamous cell carcinoma antigen 2
(Species Homo sapiens (man)
C'Date: 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 15-Sep-2003
C'Accession: 138202; 866675; 87522
C'Accession: 138202; 866675; 877522
R'Schneider, S.S.; Schick, C., Pist, K.E.; Miller, E.; Pena, J.C.; Treter, S.D.; Hui, S. Proc. Natl. Acad. 82: 01. U.S.A. 92; 3147-315; 1995
Ayfitler A serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication of A;Reference number: 138200; MUD:95241462; PMID:7724531
A;Accession: 138202
A;Status: nucleic acid sequence not shown
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A, Residues: 1-390 < SCHI.
A, Cross-references: EMBL:119576; GB:U19569; NID:G852466
R, Barnes, R.C.; Worrall, D.M.
EMBL Lett. 373, 61-65, 1995
A, Title: Identification of a novel human serpin gene; cloning sequencing and expression
A, Reference number: S66675; MUID:96013887; PMID:7589435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 LIIILPAEGMDIEEVEKLITAQQILKW--LSEMQEEEVEISLPRFKVEQKVDFKDVLYSL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 NITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSLAQS-- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 ------AGEEFLVLKSFCSAISEKKOEFTFNLANALYLOEGFTVKEOYLHGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 BFFQSAIKLVDFQDA-KACAEMISTWVERKTDGKIKDMFSGBEFGPLTRLVLVNAIYFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 QWEKKFINKEDIKEEKFWPNKNTYKSIQMARQY - - ISFHFASLEDVQAKVLEIPYKGKDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 AQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETS-
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A,Residues: 7-351,'V',353-384 <BAR>
A,Cresidues: 7-351,'V',353-384 <BAR>
C,Genetics:
                       Cross-references: GB:S66896; NID:g239551; PIDN:AAB20405.1; PID:g239552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 650; DB 2;
llarity 35.1%; Pred. No. 9.9e-36;
Conservative 90; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 STNEEFHCNHPFLFFIRONKTNSILFYGRFSSP 390
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Best Local Similarity
Matches 138; Conservat
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A;Residues: 1-191 «CRO»
A;Cross-references: UNIPROT:Q63547; EMBL:Z30585; NID:g510193; PIDN:CAA83060.1; PID:g5101
C;Superfamily: Serpin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 LSEMQEEEVEISLPRFKVEQKVDFKDVLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQK 334
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                                                                                                                                                                                                                   RESULT 2
S49162
S49162
S6-210 control of the contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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squamous cell carcinoma antigen 1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.0%
Matches 137; Conservative
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셤 8 g  $\overset{\sim}{\circ}$ g

187

64

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Durbumin-related Y protein - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: J7-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: A01244
R;Heilig, R.; Muraskowsky, R.; Kloepfer, C.; Mandel, J.L.
Nucleic Acids Res. 10, 4353-4382, 1982
Nucleic Acids Res. 10, 4353-4389, RID:7122240
A;Reference number: A01244
A;Reference number: A01244
A;Residues: 1-388 cHEI>
A;Ccoss.references: UNIPROT:P01014; GB:J00922; GB:V00439; NID:G212899; PIDN:AAA68882.1,
C;Coss-references: UNIPROT:P01014; GB:J00922; G
  inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LRTVEKELTYEKFVEWTRLDNMDEEEVEVSLPRFKLEESYDMESVLRNLGMTDAFELGKA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLSGIIDSSEVYVSQVIQKVFFEINEDGSEAAISTGIHIPVIMSLAQSQFI----ANHPF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEEFLVLKSFCSAISEKKQ---EFTFNLANALYLQEGFTVKEQYLHGNKEFFQSAIKLVD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 IBEVEKLITAQQILKW--LSEMQBEBVELSLPRFKVEQKVDFKDVLYSLNITEIFS-GGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQDA-KACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLINFTKKNGSTVKI PMMKALLRTKYGYFSESSLNYQVLELSYKGDEFSLIIILPAEGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EERLFKVSKNEEKPVQMMFKQSTFKKTYIGĖ--IFTQILVLPYVGKELNMIIMLPDETTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 AQKNTEFAVDLYQEVSLSHKDNIIPSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
A;Title: Identification and purification of a novel serine proteinase inhi
A,Reference number: A46672; MUID:93252826; PMID:8486644
A,Accession: A46672; MUID:93252826; PMID:8486644
A,Moceule type: protein
A,Residues: 47-60;63-81;91-98 <CO2>
A,Rayberimental source: placenta, leukemic cell line K562
A,Rayberimental source: placenta, leukemic cell line K562
A,Roberics: sequence modified after extraction from NCBI backbone
C,Genetics: A,Roberic GDB:DESCOS; OMIM:173321
A,Map position: 6p25-6p24.3
C,Guperianily: Serpin
C,Keywords: blocked amino end; cytosol; serine proteinase inhibitor
F;341/Inhibitory site: Arg (thrombin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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29.5%; Score 586; DB 1; Length 388;
Best Local Similarity 32.5%; Pred. No. 1.7e-31;
Matches 125; Conservative 95; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%; Score 589; DB 1; Length 37 ilarity 35.4%; Pred. No. 1e-31; Conservative 85; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIMMGHNPTESILFMGRVTNP 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGEEFLVLKSFCSAISEKKOEFTFNLANALYLQEGFTVKEQYLHGNK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFFQSAIKLVDFQDA-KACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFYQTSVESTDFANAPEESRKKINSWVESQINEKIKNLFPDGTIGNDTTLVLVNAIYFKG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSL---NYQVLELSYKGD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 RTMGMVNIFNGDADLSGMTWSHGLSVSKVLHKAFVEVTEEGVEAAAATAV---VVFELSS 356
                                                  A,Cross-references: GDB:636556; OMIM:600518
A,Map position: 18q21.3-18q21.3
A;Introns: 55/3; 74/3; 117/3; 157/1; 204/3; 256/3
A;Introns: 55/3; 74/3; 117/3; 157/1; 204/3; 256/3
C;Superfamily: Serpin
C;Keywords: glycoprotein; serine proteinase inhibitor
F;1-22/Domain: signal sequence #status predicted <SIG>F;23/20main: signal sequence #status predicted <AMT>F;55,93,170,376/Binding site: carbohydrate (Asn) (covalent) #status predicted F;354/Inhibitory site: Leu (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFSLIIILPAEGMDIEEVEKLITAQQILKW--LSEMQEEEVEISLPRFKVEOKVDFKDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 DLSMIVLLPNEIDGLQKLEEKLTABKLAMBWISLQNMRETCVDLHLPRFKXEBSYDLKDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEANTKEMFDLFQQFRKSKENNIFYSPISITSALGMVLLGAKDNTAQQISKVLHFDQVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                        23 AQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETS-
                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                          32.0%; Score 635; DB 2; Length 390; 35.0%; Pred. No. 9.7e-35; Live 90; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- OSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STNEEFCCNHPFLFFIRQNKTNSILFYGRFSSP 390
                    Gene: GDB:SCCA2; PI11
Cross-references: GDB:636556; OMIM:600518
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 138; Conserv
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plasminogen activator inhibitor type 1 precursor - American mink
C;Species: Mustela vison (American mink)
C;Species: Mustela vison (American mink)
C;Species: Mustela vison (American mink)
C;Species: Mustela vison (Bereine in 08-Feb-1996 #text_change 09-Jul-2004)
C;Accession: JG4265
R;Chuang, T.H.; Hamilton, R.T.; Nilsen-Hamilton, M.
A;Title: Cloning of the mink plasminogen activator inhibitor type-1 messenger RNA: A;Reference number: JG4265, MUID:96032362; PMID:7557448
A;Recession: JG4265
A;Rocession: JG4265
A;Residues: 1-400 cCHU5
A;Residues: 1-400 cCHU5
A;Cross-references: UNIPROT:P50449; EMBL:X58541; NID:91164923; PIDN:CAA41433.1; PID:9116
C;Comment: This protein controls the activities of the plasminogen activators and plasmi
                   GEBFLVLKSFCSAISEKKOEFTFNLANALYLQEGFTVKEQYLHGNKEFFQSAIKLVDFQD 142
                                                                                                                                                                                                                                                       GGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSLAQSQFIANHPFL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Keywords: glycoprotein; plasminogen activator; serine proteinase inhibitor F:1-21/Domain: signal sequence #status predicted <SIG> F:22-400/Product: plasminogen activator inhibitor type 1 #status predicted <P:22-400/Product: plasminogen activator inhibitor type 1 #status predicted <P:20.206.286,350/Binding site: carbohydrate (Asn) (covalent) #status predicted F:367/Inhibitory site: Arg (plasminogen activator) #status predicted
                                                                                  EDIHSRFQSLNADINKPGAPYILKLANRLYGEKTYNFLADFLASTQKMYGAELASVDFQQ
                                                                                                                                                                                                  AKACA-EMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKEDTQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PFRLNKKDTKTVK--MMYQKKKFPYNYIED--LKCRVLELPYQGKELSMIILLPDDIEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 GMDIBEVEKLITAQQILKWL--SEMQBEEVEISLPRFKVEQKVDFKDVLYSLNITEIFS-
                                                                                                                                                                                                                                                                                                                                                                                202 NF--TKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVLELSYKGDEFSLIIILP----AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 STGLEKIEKOLTLEKLREWTKPENLYLAEVNVHLPRFKLEESYDLTSHLARLGVQDLFNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 GEEFGPLIRLVLVNAIYFKGDWKOKFRKEDIQLINFIKKNGSIVKIPMMKALLRTKYGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 RGTVDQLTRLMLVNALYFNGQWKTPFPKSGTHHRLFHKSDGSTVSVPMMAQTNKFNYTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 S-ESSLNYQVLELSYKGDEFSLIIILPAE-GMDIEEVEKLITAQQILKWLSEMQEEEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDŢIFLWSLILLFFGSQASRC----SAQKNTEFAVDLYQEVSLSHKD-NIFSPLGITL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 FFIRHNPSANILFLGRFSSP 379
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Best Local Similarity
Matches 137; Conserv
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C, Superfamily: Serpin
                   83
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A.Accession: A2726
A.Accession: A2726
A.Accession: A2726
A.Accession: A2726
A.Accession: A37276
A.Accession: A37276
A.Accession: A34062
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leukcoyte elastase inhibitor - horse

ly Alternate names: plamminogen activator inhibitor-2 homolog

species: Bquus caballus (domestic horse)

c; Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

c; Accession: A42421; A37276; 53466.

B; Dubin, A.; Travis, J.; Enghild, J.; Potempa, J.

J. Biol. Chem. 267, 6576-6583, 1992 J.J.; Potempa, J.

A; Title: Equinne leukcoyte elastase inhibitor. Primary structure and identification as a A; Accession: A42421; MUID:92202200; PMID:1551869
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                                                     128 GGVEEVNFKTAAEBARQLINSWVERETNGQIKDLINSSSIDFG--TTWVFINTIYFKGIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOKFRKEDTOLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVLELSYKGDEFSLI
                                                                                                                                                                                        EEFL -- VLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYLHGNKEFFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 KIAFNTEDTREMPFSMTKEESKPVQMM---CMNNSFNVATLPAEKMKILELPYASGDLSML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 IILPAAGMDIBEVEKLITAQQILKWLS--EMQEBEVEISLPRFKVEQKVDFKDVLYSLNI
NTBFAVDLYQEVSLSH-KDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLK-QQETSAG
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29.1%; Score 577.5; DB 2;
Best Local Similarity 35.5%; Pred. No. 6e-31;
Matches 135; Conservative 86; Mismatches 138;
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DHPFLFFIRYNPTNAILFFGRYWSP 388
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A, Molecule type: protein
A, Residues: 1-379 < DUB1>
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107 114 167

62 54

227 234 285

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plasminogen activator inhibitor 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35032; JT0490; Ā60581; A39120
B;Brucdzinski, C.J.; Riordan-Johnson, M.; Nordby, E.C.; Suter, S.M.; Gelehrter, T.D.
J. Biol. Chem. 265, 2078-2085, 1990
A;Title: Isolation and characterization of the rat plasminogen activator inhibitor-1 ge:
A;Reference number: A35032; MUID:90130456; PMID:2298740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1.379 cRRNA
A;Cross-references: UNIPROT:P30740; EMBL:M93056
A;Cross-references: UNIPROT:P30740; EMBL:M93056
B;Packard, B.Z.; Lee, S.S.; Remold-O'Donnell, E.; Komoriya, A.
Biochim: Biophys: Acta 1269, 41-50, 1995
A;Title: A serpin from human tumor cells with direct lymphoid immunomodulatory
A;Reference number: 865750; MUID:96049524; PMID:7578269
A;Accession: S§5750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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A/Molecule type: protein
A/Rosidues: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
A/Rosidues: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
A/Gene: GDB:ELANH2; EI; PI2
A/Gene: GDB:ELANH2; EI; PI2
A/Cross-references: GDB:132914; OMIM:130135
A/Rosiduerfamily: Serpin
C/Superfamily: Serpin
C/Keywords: serine proteinase inhibitor
elastase inhibitor - human
C.Species: Homo sapiens (man)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: S27383, S65750
R.Remold-O'Donnell, E.; Chin, U.; Alberts, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 5635-5639, 1992
A;Title: Sequence and molecular characterization of human monocyte/neutrophi
A;Reference number: S27383; MUID:92302296; PMID:1376927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 RINKKORKTUK--MYQXKKFAYGYIED--LKCRVLELPYQGBELSMVILLPDDIEDEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 NTRFALDLFLALSENNPAGNIFISPFSISSAMAMVFLGTRGNTAAQLSKTF--HFNTVEE
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Mismatches 143;
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IRHNSSGSILFLGRFSSP 379
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Best Local S:
Matches 132
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                                                                                                                                                                                                                                                                                                                                                                                                         proteinase inhibitor nexin I precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Uul-2004
C;Accession: 148171; S70772; S35731
R;Vassalli, JD.; Huarte, J; Bosco, D.; Sappino, A.P.; Sappino, N.; Velardi, A.; Wohlwe
EMBO J. 12, 1871-1878, 1993
A;Title: Protease-nexin I as an androgen-dependent secretory product of the murine semin
A;Accession: 148717
A;Accession: 148717
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Rolecture Cype: Mixth A/Rolecture Cype: DNA A/Rolecture Cype: Mixth Cype: Mi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKEQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEF-GPLTRL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLVNALYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYF-SESSLNYQV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LELSYKGDEFSLIIILPAE-GMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 IELPYHGESISMLIALPTESSTPLSAIIPHITTKTIDSWMNTWVPKRMQLVLPKFTAVAQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDFKDVLYSLNITEIFS-GGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
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                                                                                                                295 VLPKFSLESEVNLRGPLENLGMTDMFRPNQADFSSLSDQBALYVSQALQKVKIEVNESGT 354
          STPEGRYYDILELPYHGDTLSMFIAAPYEKDVPLSALTNILDAQLISQWKGNMTRRLRLL 294
                                                                           SLPRFKVEOKVDFKDVLYSLNITEIF-SGGCDLSGITDSSEVYVSQVTQKVFFEINEDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDTIFLWSLLLLFFGSQASRCSAQK-NTEFAVDLYQEVSLSH-KDNIIFSPLGITLVLEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFT
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                                                                                                                                                                                                                                           DB 2; Length 397;
                                                                                                                                                                                                      EAATSTGIHIPVIMSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP
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Best Local Similarity 33.4%; Pred. No. 9.3e-31;
Matches 134; Conservative 93; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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A;Creater 1972 Carry And A;Creater 1972 Carry A; Gelehrter, T.D. Gene 73, 459-468, 1988
A;Title: Cloning and sequencing of cDNA for the rat plasminogen activator inhibitor-1. A;Reference number: J70490; MUID:89211983; PMID:3149611
A;Accession: J70490
A;Accession: J70490
A;Accession: J402 cZEH>
A;Cross-references: GB:M24067; NID:9577500; PIDN:AAAS6856.1; PID:9577501
A;Cross-references: GB:M24067; NID:9577500; PID:9577501
A;Cross-refe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 24-48 <NEW>
Kylson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, M.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991
A;Title: Anglocensin II induces secretion of plasminogen activator inhibitor 1 and a tis
A;Reference number: A39120; MUID:91156719; PMID:2000398
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C; Superfamily: Serpin
C; Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-402/Product: plasminogen activator inhibitor-1 #status experimental <MAT>
F;88,232,289,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;369/Inhibitory site: Arg (plasminogen activator) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVKEQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANGEMPHEFKLERTTVKQVDFSEVERARFIINDWVERHTKGMISDLLAKGAVNELTRL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLVNALYENGOWKTPFLEASTHORLFHKSDGSTISVPMMAQNNKFNYTEFTTPDGHEYDI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LELSYKGDEFSLIIILPAE-GMDIBEVEKLITAQQILKWLSEMQEBEVEISLPRFKVEQK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TIFLWSLLLLFFGSQASRC----SAQKNTEFAVDLYQEVSLSHKD-NIIFSPLGITLVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A60581; MUID: 90276328; PMID: 2190800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.7%;
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Matches 133; Conservative 8
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 24-43,'G' <ols
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A60581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
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C,Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57488
R;Sun, J; Rose, J.B.; Bird, P.
J. Biol. Chem. 270, 16089-16096, 1995
A;Thle: Gene structure, chromosomal localization, and expression of the murine homologul A;Reference number: A57488; MUID:95332310; PMID:7608171
A;Accession: A57488
A;Accession: A57488
A;Accession: A57488
A;Accession: A57488
A;Accession: A57488
A;Accession: A57488
A;Cross-references: UNIPROT:Q60854; GB:U25844; NID:g818902; PIDN:AAA79684.1; PID:g818903; A;Gene: Spi3
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A; Residues: 1-397 <SOM>
A; Residues: 1-397 <SOM>
A; Residues: 1-397 <SOM>
A; Cross-references: Unbroaded the codon TGG for residue 156 as Thr
A; Orote: the authors translated the codon TGG for residue 156 as Thr
B; Nick, H.; Hofsteenge, J.; Shaw, E.; Rovelli, G.; Monard, D.
Biochemistry 29, 2417-2421, 1990
A; Title: Functional sites of glia-derived nexin (GDN): importance of the site reacting 'A; Reference number: A34538; WUID:90248459; PMID:2337608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  members
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDA-KACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKEDTQ 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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NiAlternate names: glia-derived nexin (GDN)
CiSpecies: Rattus norvegicus (Norvesia)
CiSpecies: Rattus norvegicus (Norvesia)
CiSpecies: Rattus norvegicus (Norvesia)
CiSpecies: Rattus norvegicus (Norvesia)
CiSpecies: Autori 1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
CiSpecession: B27466, A34538; A42351; B42351; C42351
Risommer, J.; Gloor, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Meier, R
Biochemistry 26, 6407-6410, 1987
A; Telle: CDNA sequence coding for a rat glia-derived nexin and its homology
A; Reference number: A90519; MUID:88107544; PMID:3427015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 EANGTFALNILKILGEDSSKNVFLSPMSISSALAMVFMGAKGTTASQMAQALALDKCSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 EMPEKVSKNEEKPVQMMFKKSTFKMTYIGE--IFTKILLIPYVSSELNMIIMLPDEHVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 SGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSLAQSQFIANHPFLFIMKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 OKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GGGDVHQGFQSLLTEVNKTGTQYLLRTANRLFGDKTCDLLASFKDSCLKFYEAELEELDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 LINFTKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVLELSYKGDEFSLIIILPAEGMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 13
C;Superfamily: Serpin
C;Reywords: serine proteinase inhibitor
F;343/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.6%; Score 569; DB 2; Length 37 Best Local Similarity 33.6%; Pred. No. 2.2e-30; Matches 126; Conservative 82; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 VKTNGILFCGRFSSP 378
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Status: preliminary

A57488 proteinase inhibitor Spi3 - mouse C;Species: Mus musculus (house mouse)

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28.2%; Sco
32.7%; Pre
cive 97;
                                     Query Match
Best Local Similarity 32.7%
Matches 126; Conservative
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C;Superfamily: Serpin
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                                                                                   nexin/protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FS-GGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSLAQSQ---FI 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEF-GPLTRLVLVNAIYFKGDWKQK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYP-SESSLNYQVLELSYKGDEFSLIII 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOPENTKKRTFVAGDGKSYQVPMLAQLSVFRSGSTKTPNGLWYNFIELPYHGESISMLIA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEPSKANFAKITRSESLHVSHILQKAKIEVSEDGTKAAVVT----TAILIARSSPPWFI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQASRCSAQK-NTEPAVDLYQEVSLSH-KDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #text change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYLHGNKEFFQS
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                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 317-333 (ROV3>
A,Note: sequence extracted from NCBI backbone (NCBIP:93856)
A,Note: sequence extracted from NCBI backbone (NCBIP:93856)
A,Note: peptide sequences were determined from rat cDNA cloned and expit C,Superfamily: Serpin
C;Keywords: glycoprotein; serine proteinase inhibitor
E;1-20/Domain: signal sequence #status predicted <NAT>
F;1-30/Domain: proteinase inhibitor nexin 1 #status predicted <NAT>
F;159/Binding site: carbohydrate (Asn) (covalent) #status predicted
    Molecule type: protein
Residues: 364-394 <NIC>
Residues: 364-394 <NIC>
Rovelli, G.; Stone, S.R.; Guidolin, A.; Sommer, J.; Monard, D.
cochemistry 31, 3542-3549, 1992
inthe: Characterization of the heparin-binding site of glia-derived
Reference number: A42351; MUID:92207980; PMID:1554734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig.
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                                                                                                                                                                                                                  A;Molecule type:-protein
A;Residues: 165-178 <ROV2>
A;Note: sequence extracted from NCBI backbone (NCBIP:93851)
A;Accession: C42851
A;Accession: A333 <ROV3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serpin - pig

C.Species: Sus scrofa domestica (domestic pig)

C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_ch

C.Accession: 838962

R.Teschauer, W.F.; Mentele, R.; Sommerhoff, C.P.

Eur. J. Biochem. 217, 519-526, 1993

A,Title: Primary structure of a porcine leukocyte serpin.

A,Aceference number: 838962; MUID:94039085; PMID:7901009

A,Accession: 838962

A,Status: preliminary

A,Rolecule type: Protein

A,Rolecule type: Protein

A,Rosiques: 1-378 <TES>

A,Note: the sequence from Fig. 6 is inconsistent with that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is inconsistent with that
                                                                                                                                                                                        (NCBIP:93846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.3%; Score 562.5; DB 2; 33.2%; Pred. No. 6.2e-30; attive 91; Mismatches 150;
                                                                                                                                                                                        backbone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANHPFLFIMKHNPTESILFMGRVTNP
  A; Molecule type: protein
A; Residues: 364-394 «Nuc>
R; Rovelli, G.; Stone, S. R.; Guidolin, A
B; Biochemistry 31, 3342-3549, 1992
A; Title: Characterization of the heparin
A; Reference number: A42351; MUID:9220799
A; Accession: A42351
A; Molecule type: protein
A; Residues: 82-96 «ROVI>
A; Residues: 82-96 «ROVI>
A; Accession: B42351
A; Accession: B42351
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Matches 128; Conservative
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Best Local
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A; Experimental source: splice form alpha
R; Sommert J.; Gloor, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Meier, R.; Monard,
R; Sommerty 26, 6407-6410, 1987
A; Title: cDNA sequence coding for a rat glia-derived nexin and its homology to members
A; Reference number: A90519; MUID:88107544; PMID:3427015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDF-QDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 ---AEGMDIEEVEKLITAQQILKWL--SEMQEEEVEISLPRFKVEQKVDFKDVLYSLNIT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 SIEDESTGLRKIEQHITLEKLREWTKPDNIELLEVNVHLPRFRLEESYDLNAPLARLGVQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATST-GIHIPVIMSLAQSQFIA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::| ||:|:::::::|:| || ||:||:|| || 353
                                                                                                                                                                                                                                                                                                                                                                                                          85 EFLVLK-----SFCSAISEKKQEFTFNLANALYLQEGFTVKEQYLHGNKEFFQSAIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 HFDTVKDIHSRFQSLNADINKCGASYILKLANRLFGEKTYHFLPEFLASTQKTYGAELAS
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A,Accession: A26061
A,Molecule type: protein
A,Restidues: 1-259, 56, 261-398 <GLO>
R,Scott, R.W.; Bergman, B.L.; Bajpai, A.; Hersh, R.T.; Rodriguez, H.; Jone J. Biol. Chem. 260, 7029-7034, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 DIQLINF -- TKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVLELSYKGDEFSLIIILP-
                                                                                                                                                                                                     26 NTEFAVDLYQEVSLSH-KDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETSAGE
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A;Molecule type: mRNA
A;Residues: 1-328, R'. 331-398 <SOM>
A;Cross-references: GB:M17783; NID:g183063; PIDN:AAA35883.1; PID:g183064
R;Gloor, S.; Odink, K.; Guenther, J.; Nick, H.; Monard, D.
Cell 47, 687-693, 1986
                                                                                                  32;
                                                                                                                                                                                                                                                                 Length 378
Score 561; DB 2; I
Pred. No. 7.3e-30;
7; Mismatches 130;
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DHPFIFFIRHNPSSNILFLGRLSSP 378
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A Accession: A24051
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 20-47 <SCO>
C; Genetics:
A; Gene: GDB: P17; PNI
A; Cross-references: GDB:378380; OMIM:177010
A; Cross-references: GDB:378380; OMIM:177010
A; Map position: 2q33-2q35
C; Neywords: alternative splicing; glycoprotein; serine proteinase inhibitor
F; 1-19/Domain: signal sequence #status predicted <SIG>F; 20-398/Product: glia-derived nexin I, splice form beta #status experimental <MATA>
F; 20-398/Product: glia-derived nexin I, splice form alpha #status predicted
F; 10-19/Domain: signal sequence #status predicted
F; 10-19/Domain: Associate: glia-derived nexin I, splice form alpha #status predicted
F; 10-19/Diatory site: Arg (thrombin, urokinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 EMVQLGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 RLVLVNAIYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFS-ESSLNY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 RIVLVNAVYFKGIMKSRFQPENTKKRTFVAADGKSYQVPMIAQLSVFRCGSTSAPNDLWY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 QVLELSYKGDEFSLIJILPAE-GMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVE 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WHLPLFLIASVTLPSICSHFNPLSLEELGSNTGIQVFNQIVKSRPHDNIVISPHGIASVJ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
28.1%; Score 558; DB 2; Length 398;
Best Local Similarity 32.7%; Pred. No. 1.2e-29;
Matches 132; Conservative 90; Mismatches 156; Indels 26; Gaps
fitle: Protease nexin. Properties and a modified purification procedure. Reference number: A24051; MUID:85207723; PMID:3997857 . A24051
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Search completed: October 21, 2004, 06:46:13 Job time : 41 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 21, 2004, 06:33:26; Search time 193 Seconds
(without alignments)

1168.637 Million cell updates/sec

Title:

Perfect score: 1987
```

Title: US-10-628-395-2
Perfect score: 1987
Sequence: 1 MDTIFLWSLLLFFGSQASR......FIMKHNPTESILFMGRVTNP 392
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Gapop 10.0 , Gapext 0.5 Searched: 1825181 segs, 575374646 residues Total number of hits satisfying chosen parameters: 1825181

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Listing first 45 summaries
Database : Uniprot 02:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

091888 mus musculu 0691r7 xenopus lae 0995r4 home sapien 09035 gallus gall 0911d2 rattus norv Aah61536 rattus no 035684 mus musculu Bac27727 mus muscu 063547 rattus mory P29508 home sapien Aap3394 home sapien Q86w04 home sapien Q86w05 home sapien Q66w05 home sapien Q96w05 home sapien Q9byf7 home sapien Q9byf7 home sapien Q9byf7 home sapien Q9byf7 mus musculu Q6ukz2 mus musculu Q6ukz2 mus musculu Q6ukz2 mus musculu Q9dqqqq mus musculu Q9dqqq musculu Q9dqqq mus musculu Q9dqqq mus musculu Q9dqqq mus musculu Q9dqqq musculu Q9dqqq musculu Q9dqqq musculu Q9dqqq musculu Q9dqqq musqua musculu Q9dqqq musculu Q9dqqqq musculu Q9dqqq musculu Q9dqq musculu Q9dqq musculu Q9dqq musculu Q9dqq musculu Q9dq Aag97848 brachydan Q8bk60 mus musculu Q9d788 mus musculu Q8bg86 mus musculu Aah63756 mus muscul 075830 homo sapien Description SUMMARIES NEUS MOUSE BAC27727 BAC34756 Q63547 SCC1 HUMAN AAP35394 Q86W04 SPI2 HUMAN SPI2\_MOUSE QGGLT7 NEUS HUMAN NEUS\_CHICK NEUS\_CATC AAH61536 NEUS\_RAT ÕBIXI3 SCC2 HUMAN Q6HA07 Q86W05 Q86W03 Q9BYE7 Q8BHL1 Q6UKZ2 Q9D1Q2 AAR89288 Q6TGU1 AAQ97848 Q8BK60 Q9D7S8 Q8BG86 AAH63756 DB န Query Match Length D 1524 828.5 762.5 762.5 757.5 757.5 757.5 649 649 649 636 Score Result No.

002739 bos taurus Q922g2 mus musculu 008804 mus musculu	Aah61050 mus muscu Q96p63 homo sapien Q7z2y7 homo sapien	p35237 homo sapien Aah69596 homo sapi Q96p15 homo sapien P01014 qallus gall	Q6p9u0 rattus norv Aah60594 rattus no Q6ukz0 mus musculu Aar89290 mus muscu
PT16 BOVIN Q9Z2G2 O08804	AAH61050 SB12_HUMAN Q7Z2 <u>Y</u> 7	PT16 HUMAN AAH69596 SB11 HUMAN OVAY CHICK	Q6 P9 <u>U</u> 0 AAH60594 Q6UKZ0 AAR89290
100	2 1 2	- 2	0000
378 388 377	377 405 409	3 9 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	379 379 387 387
30.4 30.4 30.4	30.4 30.4 29.9	0 0 0 0 0	22000
604 604 603.5	603.5 603.5 595	0 0 0 0 0 0 0 0 0 4 0 0 0	579.5 579.5 578.5 578.5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLV 180
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                                                                                                                                                                                                                                                                                                                      MIM; 605587;

GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; TAS.
GO; GO:0006928; P:cell motility; TAS.
GO; GO:0006928; P:cell motility; TAS.
InterPro; IPR000215; Proc_inh_serpin.
PFam; PF00079; SERPIN; 1.
SWART; SW00093; SERPIN; 1.
Glycoprotein; Serrine protease inhibitor; Serpin; Signal.
SIGNAL
1 18 Social Serpin Serpin; Serpin; Serpin; Serpin; Signal.
CHAIN 19 405 Serpin I.
D. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
SUBSCELLULAR LOCATION: Secreted (Probable).
TISSUB SPECIFICITY: Expressed in pancreas and adipose tissues.
SIMILARITY: Belongs, to the serpin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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357 358 Reactive bond (By similarity).
202 202 N-linked (GlCNAc. .) (Potential).
203 N-linked (GlCNAc. .) (Potential).
306 306 N-linked (GlCNAc. .) (Potential).
405 AA, 46145 MW; 5BA18C60E4FDE9A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.2%; Score 1972; DB 1; Length 405; 99.5%; Pred. No. 5.6e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                     EMBL, AB006423; BAA33766.1; -. EMBL, AF130470; AAD34723.1; -. EMBL, BC027859; AAH27859.1; -. HSSP; P05120; LJRR.
                                                                                                                                                                                                                                                                                                             HGNC:8945; SERPINI2.
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Best Local Similarity 99.5
Matches 390; Conservative
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ID SPI2_MC
AC Q9JK88
DT 28-FEB
DT 28-FEB
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DE Ge-UU-2004 (Bartle processe inhibitor)

SERVIN IN PRESENTATION (BARTLE PROCESSE INHIBITOR)

SERVIN IN PROCESSE (STROMMASSE)14,

SUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)15,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)15,

RUB MESSESPINIS (STROMMASSE)15,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)15,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)14,

RUB MESSESPINIS (STROMMASSE)14,

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RUB MESSESPINIS (STROMMASSE)15,

RUB MESSESPINIS (STROMMASSE)15,

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SEQUENCE FROM N.A.

TISSUE=Brain,

MEDINE=22388257; PubMed=12477932;

MEDINE=22388257; PubMed=12477932;

A Itausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Itachul S.F., Zeeberg B. B., Buttow K.H., Schaefer C.F., Bhat N.K.,

A Atschul S.F., Zeeberg B. B., Buttow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Torshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Shevochenko Y., Bouffard G.G.,

Raches S.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                                                              LGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSALSEKKQEFTFNLANALYLQEGFTVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKGDEFSLIIILPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVDFKD 300
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                     BAB24976).
(in Ref. 2; BAB24976).
BAB24976).
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                                                                                                                                                                                                                       1 MDTIFLWSLLLLEFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ
                                                                                                                                                                                                                                                                                                                                                                                                      EQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEBFGPLTRLVLV
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia; Batzachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                               .
                                                                                                                               76.7%; Score 1524; DB 1; Length 405; 75.5%; Pred. No. 1e-94; ive 40; Mismatches 56; Indels
                                                                                         CRC64;
K -> T (in Ref. 2; B?
D -> S (in Ref. 2; B?
CVPMMA -> EVPTDEV (:
KVPMMA -> Y (in Ref. 2; B.
Y, 04DF38BE8545DFA8 CI
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207 D
218 KV
246 F
45775 MW;
                                                                                                                          Ouery Match
Best Local Similarity 75.5
Marches 296; Conservative
    195
207
212
246
405 AA;
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[1]
  CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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Q6GLT7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 FKDVLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVI
full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor;
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15-JUL-1998 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuroserpin precursor (Protease inhibitor 12).
Name-SERPINI; Synonyms-P112;
Name-SERPINI; Synonyms-P112;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                               Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Hypothetical protein; Protease inhibitor; Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.7%; Score 828.5; DB 2; Length 42.0%; Pred. No. 9.5e-48; ive 95; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 AA; 46392 MW; 1C53BAF8D3F72480 CRC64;
Generation and initial analysis of more than 15,000
                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397
                                                                                                                                                                                                                                                                          TISSUE=Brain;
Klein S., Strausberg R.;
submitted (JUN-2004) to the EMBL/GenBank/DDBJ
-!-SIMILARITY: Belongs to the serpin family.
EMBL; BCO74366; AAH74366.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP
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                                                                                                                     MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                SEQUENCE FROM N.A.
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099574;
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TAS.

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PROSITE; PS00284, SERPIN; 1.
Disease mutation; Glycoprotein; Serine protease inhibitor; Serpin;
                                                             GO, GO:0004867; F:serine-type endopeptidase inhibitor activity; GO; GO:0007417; P:central nervous system development; TAS. GO:0007422; P:peripheral nervous system development; TAS. InterPro; IPR000215; Prot_inh_serpin. Pfam; PF00079; Serpin, 1. SMRI; SM00093; Serpin, 1. PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                              70 K
326 S
46427 MW;
EMBL; BC018043; AAH18043.1;
HSSP; 035684; 1JJO.
                 035684; 1JJO.
: HGNC:8943; SERPINI1.
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410
363
157
401
401
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410 AA;
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Matches 155; Conserv
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362
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321
401
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                                                 MIM; 602445; -.
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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SIGNAL
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Davis R.L., Shrimpton A.E., Holohan P.D., Bradshaw C., Feiglin D.,
Davis R.L., Shrimpton A.E., Holohan P.D., Becker L.M., Lacbawan F.,
Rolins G.H., Sonderegger P., Kinter J., Becker L.M., Lacbawan F.,
Rrasnewich D., Muenke M., Lawrence D.A., Yerby M.S., Shaw C.M.,
A Gooptu B., Elliott P.R., Finch J.T., Carrell R.W., Lomas D.A.;
"Familial dementia caused by polymerization of mutant neuroserpin.";
In Nature 401:376-379(1999)
C. - FUNCTION: Serine protease inhibitor that inhibits plasmingen activators and plasmin but not thrombin. May be involved in the formation or reorganization of synaptic connections as well as for synaptic plasticity in the adult nervous system. May protect neurons from cell damage by tissue-type plasminogen activator.
C. - SUBCELLUIAR LOCATION: Secreted.
- InSUBSE: Defects in SERPINII are the cause of familial encephalopathy with neuroserphi inclusion bodies (FEMIB)
[MIM:604218]. FEMIB is characterized clinically as an autosomal comminantly inherited dementia, histologically by unique neuronal inclusion bodies and biochemically by polymers of neuroserpin.
C. - SIMILARITY: Belongs to the serpin family.
                                        MEDLINE=97224485; PubMed=9070919;
Schrimpf S.P., Bleinker A.J., Brecevic L., Kozlov S.V., Berger P.,
Osterwalder T., Krueger S.R., Schinzel A., Sonderegger P.; and "Human neuroserpin (PI12): cDNA cloning and chromosomal localization
                                                                                                                                                           SEQUENCE FROM N.A.
Kinter J., Berger P., Kozlov S.V., Sonderegger P.,
"Genomic organization of the human neuroserpin (PI12) gene.",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS FENIB PRO-49 AND ARG-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences."
                                                                                                                             Genomics 40:55-62(1997).
          SEQUENCE FROM N.A.
TISSUE=Retina;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Reactive bond (By similarity).
N-linked (GlorNac. .) (Potential).
N-linked (GlorNac. .) (Potential).
S -> P (in FRINB; Syracuse).
FTId=VAR 008520.
S -> R (in FENIB; Portland).
FTIG=VAR 008521.
K -> E (in Ref. 3).
S -> Y (in Ref. 3).

Potential. Neuroserpin.

D966E9036BB21943 CRC64;

64 65

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GSTQKEIRHSMGYDSLKNGEEFSFLKEFSNMVTAKESQYVMKIANSLFVQNGFHVNEEF1 125
                                                                                                                                                                                                                                                                                                                      126 QMMKKYFNAAVNHVDFSQNVAVANYINKWVENNTNNLVKDLVSPRDFDAATYLALINAVY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 YKGDEFSLIIILPAAGMDIBEVEKLITAQQILKWLSEMQBEEVEISLPRFKVEQKVDFKD 300
                                                                                                                         6 LFSLLVLQSMATGATFPEEAIADLSVNMYNRLRATGEDENILFSPLSIALAMGMMELGAQ
                                                                                                                                                                                                                                                                        HGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIY
                                                                                                                                                                                                                                                                                                                                                                    185 FKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVLELS
                                                                                                                                                                                                                                                                                                                                                                                               6 LWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKD-NIIFSPLGITLVLEWVQLGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name-SERPINII; Synonyms=PI12;
Name-SERPINII (Synonyms=PI12;
Gallus gallus (Chicken)
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSL.
                                              Gaps
                                                ņ
39.8%; Score 791.5; DB 1; Length 410; 39.5%; Pred. No. 3e-45;
                                              Indels
                                           135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 LYPQVIVDHPFFFLIRNRRTGTILFMGRVMHP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 AA
                                           97; Mismatches
                                              Conservative
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NEUS CH
Q90935;
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EMBL, Z81326; CAB03626.1; -. EMBL, AF248246; AAG01089.1; -. EMBL, AF248244; AAG01089.1; OINED. EMBL, AF248245; AAG01089.1; JOINED.

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                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Neuroserpin is expressed in the pituitary and adrenal glands and induces the extension of neurite-like processes in AtT-20 cells."; Blochem. J. 345:595-601(2000).

-1- FUNCTION: Serine protease inhibitor that inhibits plasminogen activators and plasmin but not thrombin. May be involved in the formation or reorganization of synaptic connections as well as f synaptic plasticity in the adult nervous system. May protect neurons from cell damage by tissue-type plasminogen activator (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reactive bond (By similarity).
N.linked (GlcNAc. .) (Forenti
N.linked (GlcNAc. .) (Potenti
N.linked (GlcNAc. .) (Potenti
N.linked (GlcNAc. .) (Potenti
L -> M (in Ref. 1; AAF70387).
H -> Q (in Ref. 1; AAF70387).
W, 9900862481A36608 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, 035694; JUJO.

InterPro; IPR00215; Prot_inh_serpin.

InterPro; IPR00215; Prot_inh_serpin.

SMART; SM00093; SERPIN; 1.

PROSITE; PS00284; SERPIN; 1.

Glycoprotein; Serine protease inhibitor; Serpin; Signal.

SIGNAL 17 410 Neuroserpin.

SITE 362 363 Reactive bond (By similarity).

CARBOHYD 157 157 N'linked (GlCNAc. . ) (Potent CARBOHYD 321 321 N'linked (GLCNAc. . ) (Potent CARBOHYD 321 M'LINKED CARBOHYD M'LINKED CARBOHYD 321 M'LINKED CARBOHYD M'LINKED CARBOHYD M'LINKED CARBOHYD M'LINKED CARBOHYD
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ш
                                                                                                                                                                                                           09JJD2; 09JJD1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuroserpin precursor (Protease inhibitor 17)
MSLAQSQFIANHPFLFIMMHNPTESILFMGRVTNP
                              |:: | | :||| |:::: | ::|||||| :|
MAVLYPQVIVDHPFFFLVRNRRTGTVLFMGRVMHP
                                                                                                                                                                                  410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Pituitary;
MEDLINE-20115094; PubMed=10642518;
MH111 R.M., Parmar P.K., Coates L.C., Mezey
Birch N.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF193014; AAF70386.1; -. EMBL; AF193015; AAF70387.1; -.
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                              Synonyms=Pil2;
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                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362
1157
401
112
                                                                                                                                                                                                                                                                                                                                                 Name=Serpinil;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
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     358
                                                       363
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                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSYKGDEFSLIILLPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLERFKVEQKVD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKDVLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFBINEDGSEAATSTGIHIPVI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAHGTTLKEIRHSLGFDSLKNGEEFTFLKDLSDMATTEESHYVLNMANSLYVQNGFHVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLWSLILLFFGSQASRCSAQKNT--EFAVDLYQEVSLSHKD-NIIFSPLGITLVLEMVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                        "Neuroseptin, an axonally secreted serine protease inhibitor.";

EMBO J. 15:2944-2953(1996).

-!- FUNCTION: Serine protease inhibitor that inhibits plasminogen activators and plasmin but not thrombin. May be involved in the formation or reorganization of synaptic connections as well as f synaptic plasticity in the adult nervous system. May protect neurons from cell damage by tissue-type plasminogen activator.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: In the embryo present in retina, brain, cerebellum and spinal cord. In adult, predominantly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct protein sequencing, Glycoprotein, Serine protease inhibitor; Serpin, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuroserpin.
Reactive bond (By similarity).
N-linked (GlCNAc. . ) (Potential).
N-linked (GlCNAc. . ) (Potential).
DSB3B03E77FSFCE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osterwalder T., Contartese J., Stoeckli B.T., Kuhn T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the serpin family.
                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z71930; CAA96493.1; -.
PIR; S70647; S70647.
PIRSP; O35684; JJJO.
INTEFPRO; IPRO00215; Prot_inh_serpin.
Pfam; PF00079; Serpin; 1.
PART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                               STRAIN=White leghorn; TISSUE=Brain;
MEDLINE=96272154; PubMed=8670795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 40.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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XX MEDINE-Pituteary gland;

XX MEDINE-2388257; PubMed=12477932;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZenna P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                       267
                                                                                                                                        322
                                                                                                                                                                                                                             AEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKOKFRKEDTQLINFTKK 206
                                                                                                                                                                                                          SSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSLAQSQFIANHPFLFIMKHNPTES 382
                    ANYINKWVENYTNSLLKDLVSPGDFDAVTHLALINAVYFKGNWKSOFRPENTRTFSFTKD
                                                                                        NGSTVKI PMMKALLRTKYGYFSESSLN - - - YQVLELSYKGDEFSLIILLPAEGMDIEEV
                                                                                                                                      EKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVDFKDVLYSLNITEIFSGGCDLSGITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                              AAH61536,
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Serine (Or cysteine) proteinase inhibitor, clade I (Neuroserpin),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.4%; Score 762.5; DB 2; Length 410; 39.5%; Pred. No. 2.7e-43; live 97; Mismatches 122; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46278 MW; 99008624B3A366D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                      410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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SEQUENCE 410 AA; 46278 M
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Best Local Similarity 39.5'
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                           ILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                            388 ILFMGRVMHP 397
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147
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MEDINEE FROM N.A.

MEDINEE 2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Henge L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaska W.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                  87 LVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYLHGNKEFFQSAIKLVDFQDAKAC 146
                                                                                                                                     88 SFLRDFSSMVSAEEGQYVWKIANSLFVQNGFHINEEFLQMMKMYFNAEVNHVDFSENVAV 147
                                                                                                                                                                                                                                                                                                                   148 ANYINKWVENYTNSLLKDLVSPGDFDAVTHLALINAVYFKGNWKSQFRPENTRTFSFTKD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSLAQSQFIANHPFLFIMKHNPTES 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 KKELFLSKAVHKSFIEVNEEGSEAAVASGMIAISRMAVLFPQVIVDHPFLFLIKNRKTGT 387
         87
EWSVNVYNHLRATGEDENILFSPLSIALAMGVMELGAQGSTLKEIRHSMGYESLKSGEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                      207 NGSTVKIPMMKALLRTKYGYFSESSLN----YQVLELSYKGDEFSLIIILPAEGMDIEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKEDTQLINFTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKLITAQQILKWLSEMQEBEVEISLPRFKVEQKVDFKDVLYSLNITEIFSGGCDLSGITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUB=Brain;
MEDLINE=98033339; Pubmed=9364046;
Krueger S.R., Ghisu G.-P., Cinelli P., Gschwend T.P., Osterwalder Wolfer D.P., Sonderegger P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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BAC27727;
14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430403B13 product:serine (or cysteine) proteinase inhibitor, olade I (neuroserpin), member 1, full insert sequence.
Mus musculus (Mouse).
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MEDLINE=214636364;

MEDLINE=2146364;

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EMBL; BC006776; AAH06776.1; -.

PDB; 1JJO; X-ray; A/B=25-64, C/D=101-361, E/F=367-399.

MGJ; MG1:1194260; Serpini.

InterPro; IFR00015; Prot_inh_serpin.

Pfam; PF00079; Serpin; 1.

PROSITE; PS00284; SERPIN; 1.

PROSITE; PS00284; SERPIN; 1.

3D-Structure; Glycoprotein; Serine protease inhibitor; Serpin; Signal.

SIGNAL
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Neurosezpin.
Reactive bond (By similarity).
N-linked (GlCNAc. .) (Fotential).
N-linked (GlCNAc. .) (Fotential).
N-linked (GlCNAc. .) (Fotential).
E -> G (in Ref. 2).
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MEDLINE=98113198; PubMed=9442076;
MEDLINE=98113198; PubMed=9442076;
Ostring S.P., Cinelli P., Baici A., Pennella A., Krueger S.R.,
Schring S.P., Mains M., Sonderegger P.;
"The axonally secreted serine proteinase inhibitor, neuroserpin,
inhibits plasminogen activators and plasmin but not thrombin.";
J. Biol. Chem. 273:2312-2321(1998).
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Berger P., Kozlov S.V., Krueger S.R., Sonderegger P.;
"Structure of the mouse gene for the serine protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroserpin (PI12).";
Gene 214:25-33(1998).
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Adachi U., Alzawa T., Arakawa T., Bono H., Carninci P.,
Adachi S., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi S., Furuno M., Hanagaki T., Haraka T., Hirozane T.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraaka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saitoh H., Sahinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                              STRAIN-CS7BL/6J; TISSUE-Olfactory brain, MEDLINE-22036681; PubMed=12466851; The FANTOM Consortium. The FANTOM Consortium. The RIKEN Genome Exploration Research Group Phase I & II Team, the RIKEN Genome Exploration Research Group Phase I & II Team, 07.00 full-length cDNAs."; Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1830(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/64; TISSUE-Olfactory brain; MEDLINE-20530913; PubMed=11076861; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Natshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Natsukra Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKD integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Olfactory brain;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUE=Olfactory brain; MEDLINE=9927953; Pubmed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length DNA cloning."; Meth. Enzymol. 303:19-44(1999).
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27 TEWSVNMYNHLRGTGEDENILFSPLSIALAMGMMELGAQGSTRKEIRHSMGYEGLKGGEE 86
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130073K19 product:serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=CS7BL/67; TISSUE=Spinal ganglion;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
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BAC34756
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85

Gaps

'n

27 TEFAVDLYQEVSLSHKD-NIIPSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETSAGEE

148; Conservative

Similarity

Best Local Matches 14

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NEDLINE=92068241; PubMed=1958219;
Wishir F., Sekiguchi K., Kato H.;
Squamous cell carcinoma antigen is a new member of protease inhibitors.";
                                                                                                                                                                                                                                                                                                 36.6%; Score 728; DB 2; 77.0%; Pred. No. 2.2e-41; ive 22; Mismatches 19.
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                                                                                                                                                                                                                                                                                                                    Best Local Similarity 77.0
Matches 137; Conservative
             Rattus norvegicus (Rat)
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                                                                              SEQUENCE FROM N.A.
                                                NCBI_TaxID=10116;
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Name=ZG-21;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Buchi J., Aizawa K., Hangaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu W., Hirancko K., Hiracka T., Hirozane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
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A Katoh H., Kawai J., Kojima Y., Konno H., Konno H.,
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Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume M., Sano H.,
A sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AKOS1756, BAC34756.1;
SECUENCE 410 AA, 46347 WW, DA3AF6F5195EBB7C CRC64;
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                   STRAIN=CSTBL/6J; TISSUE-Spinal ganglion;
MIDLINE=20530913; PubMed=11076861;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKE Integrated Sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000)
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Last annotation update)
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(TrEMBLrel. 26, I
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01-NOV-1996
01-MAR-2004
ZG-21p.
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kartus norvegicus (kar).
Eukaryota; hatazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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BIDLINE=L2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFFEINEDGSEAATSTGIHI PVIMSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP
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P19508; Q96021;
28-FEB-2003 (Rel. 25, Created)
28-FEB-2004 (Rel. 41, Last sequence update)
Squamous cell carcinoma antigen 1 (SCCA-1) (Protein T4-A).
Name=SERPINB3; Synonyms=SCCA1, SCCA;
                                                                                                                                                                                                                                                                   EMBL; Z30585; CAA83060.1; -. SIMILARITY: Belongs to the serpin family.

EMBL; Z30585; CAA83060.1; -. SEMBL; Z30585; CAA83060.1; -. SIMILARITY: S4162.

RISP; PO1009; LATH.

GO; GO:0004867; F:serine-type endopeptidase inhibitor act: ThterPro; IPR000215; Proc_inh_serpin.

Pram; PF00079; SSTPIN; 1. SMART; SM00093; SSRPIN; 1. SMART; SM00093; SSRPIN; 1. SMART; SM00093; SSRPIN; 1. SPOSITE; PS00284; SBRPIN; 1. SPOSITE; PS00284; SPRPIN; 1. SPOSITE; PS00284; SRRPIN; 1. SEQUENCE 191 AA; 21825 MW; 9EC312FDBD169320 CRC64;
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Cronshagen U., Chen C., Kern H.F.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heshe F.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahed J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDELBLUGGE 20413472; PubMed=10956412;
WEDELBLUGGE 20413472; PubMed=10956412;
Wemura Y., Pak S.C., Luke C., Cataltepe S., Tsu C., Schick C.,
Wemachi Y., Pomeroy S.L., Perlmutter D.H., Silverman G.A.;
"Circulating serpin tumor markers SCCA1 and SCCA2 are not actively
"Circulating serpin tumor markers SCCA1 and SCCA2 are not actively
"Circulating serpin tumor markers SCCA1 and SCCA2 are not actively
"Int. J. Cancer 89:368-377(2000)
"Int. J. Cancer 89:370(2000)
"Int. J. Cancer 89:370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew, HGNC:10569, SERPINB3.
MIM, 600517; -. GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct protein sequencing; Serine protease inhibitor; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.7%; Score 649; DB 1; Length 390; Best Local Similarity 35.3%; Pred. No. 1.2e-35; Matches 138; Conservative 89; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 T -> A (in Ref. 1).
44564 MW; ESF27F986C752CFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000215; Prot_inh_serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL, U19559, AAA86317.1; JOINED EMEL, U19562, AAA86317.1; JOINED EMEL, U19562, AAA86317.1; JOINED EMEL, U19565, AAA86317.1; JOINED EMEL, U19567, AAA86317.1; JOINED EMEL, U19559, AAA86316.1; JOINED EMEL, U19550, AAA86316.1; JOINED EMEL, U19560; AAA86316.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S66896; AAB20405.1; -.
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EMBL, BC005224, AAH0524.1;
PIR, 138201; 138201.
HSSP, P01008; LATH.
SWISS-2DPAGE; P29509; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00079, Serpin, 1.
SMART; SM00093, SERPIN, 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 AA;
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CONFLICT
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Gaps

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------AGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYLHGNK 128
                                                                                                                                                                                                                                                                                                                                                                           DWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVLELSYKGDEFS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIIILPAEGMDIBEVEKLITAQQILKW--LSEMQEEEVEISLPRFKVEQKVDFKDVLYSL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTTGKAATYHVDRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGEKTYLFLOEYLDAIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 NITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGI----HIPVIMSLA 361
                                               124
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Serine (Or cysteine) proteinase inhibitor, clade B (Ovalbumin), member
                                                                                                                                                                                                                                                                                                                               EFFQSAIKLVDFQDA-KACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKG
AQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 OWEKKFNKEDÍKEEKFWPNKNIYKSÍOMMRQY--TSPHFASLEDVQAKVLEIPYKGKDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEANTKFWFDLFQQFRKSKENNIFYSPISITSALGMVLLGAKDNTAQQIKKVLHFDQVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 AQKNTBFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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EMBL; BT006748; AAP35394.1; -.
SEQUENCE 390 AA; 44564 MW; E5F27F986C752CFA CRC64;
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Matches 138; Conservative
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AAP35394;
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                  302
  LIIILPAEGMDIBEVEKLITAQQILKW--LSEMQEEEVEISLPRFKVEQKVDFKDVLYSL 305
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                                      306 NITELFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGI----HIPVIMSLA
                                                23 AQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQLGAKGKAQQQIRQTLKQQETS-
                                                                                                                                                                                                                                                       Ol-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last sequence update)
60-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
60-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Name-SERPINB3;
Name-SERPINB3;
Fund Sapiens (Hunan)
Fundare, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                         360 NEEFHCNHPFLFFIRQNKTNSILFYGRFSSP 390
                                                                            QSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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137; Conservative
                                                                                                                                                PRELIMINARY;
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Matches 13
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248 LIIILPAEGMDIEEVEKLITAQQILKW--LSEMQEEEVEISLPRFKVEQKVDFKDVLYSL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 0004867; F:serine-type endopeptidase inhibitor activity; IEA. InterPro; IPR000215; Prot_inh_serpin.
Pfam; PF00079; Serpin; 1.
SWART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Protease inhibitor; Serine protease inhibitor; Serpin.
SEQUENCE 390 AA; 44504 MW; E9D56D2D786C9E24 CRC64;
                                                                                                                                                                        Homo sapiens (Human),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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32.2%; Score 640; DB 2; Length 390;
Best Local Similarity 34.9%; Pred. No. 4.8e-35;
Matches 137; Conservative 89; Mismatches 137; Indels
                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Squamous sell carcinoma antigen 1.
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PRELIMINARY;
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; Search time 71 Seconds (without alignments) . 1980.590 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
                                                                                                          October 21, 2004, 06:33:26
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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45	636	•	390	vo	ABB98811	Abb98811 SCCA2 pro

## ALIGNMENTS

AAW48391 standard; protein; 392 AA.

RESULT 1 AAW48391

AAW48391;

pancreas-derived; plasminogen activator; inhibitor; PAPAI; diagnosis; treatment; disorder; cancer; blood coagulation; viral infection; pregnancy complications; preeclampsia; intrauterine growth retardation, wound healing; tumour invasion; metastasis; leukaemia; lung; breast; endometrial; ovarian; melanoma; gastrointestinal; pancreatic; colorectal; coagulation; thrombi; arterial; venous; inflammation; antiviral; HIV-1; New isolated pancreas-derived plasminogen activator inhibitor - useful for developing products for diagnosis and treatment of disorders, e.g. cancers, blood coagulation or viral infections. Homo sapiens pancreas-derived plasminogen activator inhibitor. 1. .14 /note= "leader sequence" 15. .392 /label= mature PAPAI Location/Qualifiers 96WO-US013283 96WO-US013283 (HUMA-) HUMAN GENOME SCI INC Gentz RL, Ruben SM; (first entry) WPI; 1998-169083/15. N-PSDB; AAV17829. HIV-2; hepatitis. Homo sapiens WO9807735-A1 16-AUG-1996; 16-AUG-1996; 03-AUG-1998 26-FEB-1998 Peptide Protein Ni J, 

Claim 16; Fig 1; 88pp; English

The sequence is that of pancreas-derived plasminogen activator inhibitor

15. .392 /label= PAPAI

Protein

WO9909161-A1

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activity of the plasminogen activator (PA) system is implicated e.g. complications of prepancy such as preclampais and intractation of prepancy such as preclampais and intractarine growth retardation, cancer and wound healing. Since plasminogen activator inhibitors (PAI) inhibit tumour cell invasion and metastasis, the products provide a method for treating or preventing tumour invasion and metastasis in cancers including pleukaemia, lung cancer, breast cancer, endometrial and ovarian cancer, melanoma, and gastrointestinal cancers, including pancreatic cancer and colorectal cancer. In addition, since PAI's inhibit fibrinolysis, the products provide a method for treating or preventing coagulation disorders including arterial thrombi, venous thrombi, disseminated intravascular coagulation, and excessive bleeding caused by the administration of a pharmaceutical PA such as urokinase or tissue PA. Further, since PA's are effective antiviral agents, the products provide a method for treating or preventing infections caused by viruses including HIV-1, HIV-2 and hepatitis A, B, C, E, F, and G. The products can also be used for detection and diagnosis of the above
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New isolated pancreas-derived plasminogen activator inhibitor - useful for developing products for treating conditions such as complications of pregnancy, cancer, wound healing, coagulation disorders or virus infection.

Claim 11; Fig 1; 123pp; English.

(HUMA-) HUMAN GENOME SCI INC. (LONG-) LONG ISLAND JEWISH MEDICAL CENT.

98WO-US003217 97US-00934011

18-FEB-1998; 15-AUG-1997;

25-FEB-1999

Shi YE;

Gentz RL, Ruben SM,

Νi J,

WPI; 1999-190161/16. N-PSDB; AAX19885.

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The present sequence represents an isolated human pancreas-derived plasminogen activator inhibitor (PAPAI). PAPAI proteins inhibit plasminogen activators such as urokinase and tissue plasminogen activators such as urokinase and tissue plasminogen activators such as urokinase and tissue plasminogen activators productions in which abnormal activity of the plasminogen activator system is implicated, e.g. complications of pregnancy such as preclampia and intrauterine growth retardation, cancer, inflammation and wound healing. They can also be used for treating or preventing e.g. tumour invasion and metastasis, coagulation disorders e.g. arterial thrombi, venous thrombi, disseminated intravascular coagulation, and excessive bleeding caused by the administration of a pharmaceutical plasminogen activator, infections caused by viruses e.g. HIV-1, HIV-2, hepatitis A, B, C, E, F or G. The products can also be used for detection and diagnosis.
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Pancreas derived plasminogen activator inhibitor; PAPAI; detection; diagnosis; breast cancer; pregnancy; wound healing; coagulation disorder;

diagnosis; bream Homo sapiens.

Location/Qualifiers

Key Peptide

1. .14 /label= signal

Pancreas derived plasminogen activator inhibitor protein.

(first entry)

14-JUN-1999

AAY04120;

AAY04120 standard; protein; 392

120

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121 EQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLV
EQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLV
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19-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acids encoding pancreas-derived plasminogen activator inhibitor (PAPAI) protein. Plasminogen activator inhibitor (PAPAI) protein. Plasminogen activator inhibitor (PAI) 1 and 2 are involved in many physiological and pathological processes, including normal pregnancy, precelampsia, intrauterine growth retardation, wound healing, tumour cell invasion and merstessis, inflammatory bowel disease, appendictis, complication and arthritis, inflammarory bowel disease, and prostatic involution and osteonecrosis. PAPAI DNA is used to treat physiological and pathological conditions including breast cancer and to detect pathological disorders. PAPAI DNA is used to treat present sequence is a human PAPAI protein
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                                                                                                                                                                                                                                                                 Human, pancreas-derived plasminogen activator inhibitor, PAPAI, plasminogen activator inhibitor, PAI; preeclampsia; wound healing; intrauterine growth retardation; tumour cell invasion; arthritis; metastasis; inflammation; inflammatory bowel disease; appendicitis; systemic lupus erythematcsus; ovulation; cytostatic; gene therapy; prostatic involution; osteonecrosis; breast cancer; pregnancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides encoding the pancreas-derived plasminogen activator inhibitor protein are useful to treat physiological and pathological conditions including breast cancer, and to detect pathological disorders.
                                                                                                                                                                                                                          Human Pancreas-derived plasminogen activator inhibitor (PAPAI) #1.
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100.0%; Pred. No. 5.8e-170;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human mature PAPAI"
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'label= Signal_peptide
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                                                                                              AAE14266 standard; protein; 392 AA.
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97US-00934011
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Best Local Similarity 100. Matches 392, Conservative
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N-PSDB; AAD23710.
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15-AUG-1997;
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LGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVK 120

MDTIFLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ 60 1 MDTIFLWSLLLLFFGSQASRCSAQXNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ

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Human, pancreas-derived plasminogen activator inhibitor, PAPAI; cytostatic, vilnerary; gynecological, haemostatic; virucide; HIV, human immunodeficiency virus; gene therapy, fibrinolytic system, tumour invasion; metastasis, haemorrhage; hepatic illness; liver cancer; alcoholic cirrhosis; primary biliary cirrhosis; pre-eclampsia; eclampsia; letakaemia; breast cancer; lung cancer; coagulation disorder; arterial thrombus; venous thrombus; excessive bleeding; viral infection; hepatitis; wound healing; intrauterine growth retardation.
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/label= Mature PAPAI
/note= "Pancreas-derived plasminogen activator inhibitor"
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/label= Signal_peptide
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98US-00026408.
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Homo sapiens
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19-FEB-1998;
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                                 The invention describes an isolated pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptide (I). The polynucleotide (II) encoding (I) is useful for diagnosing a disorder involving comparing encoding (I) is useful for diagnosing a disorder involving comparing the standard expression levels in cells or body fluid of an individual with the standard expression level where an increase or decrease in the PAPAI gene expression level where an increase or decrease in the PAPAI came expression level of the individual is indicative of the disorder. Since PAPAI regulates fibrinolytic system, substantial alterations in PAPAI activity, serve as markers of tummour invasiveness and metastasis. CI is useful for predicting whether: a tumour is likely to remain stable, or the invade tissue and ultimately metastasis; a haemorrhage likely to occur in patients suffering from hepatic illness such as alcoholic carrhoesis, primary billary cirrhosis, and il a pre-eclamptic patient is at risk for developing eclampsia. (I) is useful for rasising polycional and monoclonal antibodies which are useful in diagnostic patient is useful for treating; or inhibiting tumour invasion and metastasis in cancers including e.g., leukaemia, breast cancer, lung cancer; coagulation disorders e.g., arterial thrombi, venous thrombi, excessive to bleeding and treating viral infections such as human immunodeficiency virus, hepatitis A. B. C. gord virus. (I) inhibits plasminogen activator system is implicated, e.g., complications of pregnancy such as pre-eclampsia, wound healing and intrauterine growth retardation. This is the amino acid sequence of a human pancreas-derived plasminogen activator inhibitor
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             Claim 11; Fig 1A-B; 52pp; English
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Best Local Similarity 100.
Matches 392; Conservative
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ADO05045 standard; protein; 392

(first entry)

29-JUL-2004

AD005045;

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Producing an antibody that specifically binds to pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptide comprises introducing the polypeptide to the animal, and recovering the antibody.
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0
                                                          Pancreas-derived plasminogen activator inhibitor; PAPAI; human.
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                                                                                                                                                                                                                                                                           15. .392
/note= "Human mature PAPAI protein"
                                                                                                                                                                                                                       1. .14
/label= Signal_peptide
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97US-00934011.
98US-00026408.
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Human PAPAI protein #1.
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N-PSDB; ADO05044.
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RUBEN S M.
SHI Y E.
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MDTIFLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ
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15-AUG-1997;
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360
               VLYSENITEIFSGGCDLSGITDSSEVYVSQVTQXVFFEINEDGSEAATSTGIHIPVIMSL 360
                                                                                                                                                                                                                                                                       derived plasminogen activator inhibitor, PAPAI; detection; s; breast cancer; pregnancy; wound healing; coagulation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated pancreas-derived plasminogen activator inhibitor - useful for developing products for treating conditions such as complications of pregnancy, cancer, wound healing, coagulation disorders or virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caused by viruses e.g. {\rm HIV}-1, {\rm HIV}-2, hepatitis {\tilde{A}}, B, {\rm Q} products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1987; DB 2; Best Local Similarity 100.0%; Pred. No. 6e-170; Matches 392; Conservative 0; Mismatches 0;
                                                                         AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                        AOSOFIAMHPFLFIMKHNPTESILFMGRVTNP 392
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LONG ISLAND JEWISH MEDICAL CENT.
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/label= signal
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/label= PAPAI
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N-PSDB; AAX19886.
                                                                                                                                                                                                                                                                                                    virus infection.
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                                                                                                                                                                                                                                                                                      diagnosis;
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1 MDTIFLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ
                                                                                                              LGAKGKAQQQIRQTLKQQETSAGEBFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides encoding the pancreas-derived plasminogen activator inhibitor protein are useful to treat physiological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Pancreas-derived plasminogen activator inhibitor (PAPAI)
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/note= "Human mature PAPAI"
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/label= Signal_peptide
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97US-00934011.
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N-PSDB; AAD23718.
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Location/Qualifiers

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16-AUG-1996;
15-AUG-1997;
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Peptide
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                                                             The invention relates to nucleic acids encoding pancreas-derived plasminogen activator inhibitor (PAPAI) protein. Plasminogen activator inhibitor (PAI) 1 and 2 are involved in many physiological and pathological processes, including normal pregnancy, precelampsia, intrauterine growth retardation, wound healing, tumour cell invasion and metastesis, inflammation and arthritis, inflammatory bowel disease, appendicitis, complications from systemic lugus erythematosus, ovulation and prostatic involution and osteonecrosis. PAPAI DNA is used to treat physiological and pathological conditions including breast cancer and to detect pathological and paralogical sonditions including breast cancer and to present sequence is a human PAPAI protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; pancreas-derived plasminogen activator inhibitor; PAPAI; cytostatic; vulnerary; gynecological; haemostatic; virucide; HIV; human immunodeficiency virus; gene therapy; fibrinolytic system; tumour invasion; metastasis; haemorrhage; hepatic illness; liver cancer; alcoholic cirrhosis; primary biliary cirrhosis; pre-eclampsia; elampsia; letksemia; breast cancer; lung cancer; coaqulatich disorder; arterial thrombus; venous thrombus; excessive bleeding; viral infection; hepatitis; wound healing; intrauterine growth retardation.
                                                                                                                                                                                                                                                                                                                                                    LGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISBKKQEFTFNLANALYLQEGFTVK 120
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                                                                                                                                                                                                                                                                                                   1 MDTIFLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ
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                                                                                                                                                                                                                                                                         Gaps
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pathological conditions including breast cancer, and to detect pathological disorders.
                                                                                                                                                                                                                                                  5; Length 405;
                                                                                                                                                                                                                                               100.0%; Score 1987; DB 5; Length
100.0%; Pred. No. 6e-170;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pancreas-derived plasminogen activator inhibitor #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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                                       Claim 37; Fig 4; 50pp; English.
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                                                                                                                                                                                                                                                                       392; Conservative
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                        Sequence 405 AA;
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ABG72448
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The invention describes an isolated pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptide (I). The polymucleotide (II) conclusion (II) as useful for diagnosing a disorder involving comparing (I) is useful for diagnosing a disorder involving comparing the standard expression level in relis or body fluid of an individual with the standard expression level where an increase or decrease in the PAPAI can expression level where an increase or decrease in the PAPAI is useful for predicting whether: a tumour invasiveness and metastasis.

Consider a useful for predicting whether: a tumour is likely to remain to table, or the invade tissue and ultimately metastasise; a haemorrhage likely to occur in patients suffering from hepatic illness such as alcoholic cirrhosis, primary primary plilary cirrhosis, and liver cancer; a continuous control of arthosis, primary philary cirrhosis, and liver cancer; a patient is at risk for developing eclampsia. (I) is useful for raising contain an annothal and monoclonal antibodies which are useful in diagnostic assays for detecting PAPAI protein expression, and to capture PAPAI protein expression, and to capture PAPAI concern binding proteins which are also candidate agonist or antagonist. (I) is useful for treating: or inhibiting tumour invasion and metastasis in cancers including e.g., leukaemia, breast cancer, lung cancer, coagulation disorders e.g., arterial thrombi, venous thrombi, excessive collecting and treating viral infections such as human immunodeficiency virus, the aborrant activity of plasminogen activator system, and thus is useful for treating disease conditions in which abnormal activity of plasminogen activator system is implications of pregnancy such as pre-eclampsia, wound healing and trauterine growth retardation. This is the amino acid sequence of a human pancreas-derived plasminogen activator inhibitor
                                                                                 19. .405
/label= Mature_PAPAI
/note= "Pancreas-derived plasminogen activator inhibitor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated pancreas-derived plasminogen activator inhibitor polypeptide useful for treating or inhibiting tumor invasion and metastasis in cancers, pre-eclampsia, arterial or venous thrombi.
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1. .18
/label= Signal_peptide
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97US-00934011.
98US-00026408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gentz RL, Ruben SM,
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Matches 392; Conservative
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                                                                                                                                                   LGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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                                                                                                                  LGAKGKAQQQIRQTLKQQETSAGEBFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVK
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                                                                                                                                                                                                     BOYLHGNKEFFOSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEBFGPLTRLVLV
                                                                                                                                                                                                                                                      NAIYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLNYQVLELS
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                                                                                                 MDTIFLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ
                                                                          Gaps
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                                                   405;
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                                                   Length
                                                                          Indels
                                               Score 1987; DB 8;
pred. No. 6e-170;
mismatches 0;
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                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 392; Conservative 0
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protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sarcoma;
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 inhibitor (PAPAI)
                         Sequence 405 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing an antibody that specifically binds to pancreas-derived plasminogen activator inhibitor (PAPA1) polypeptide comprises introducing the polypeptide to the animal, and recovering the antibody.
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                         180
                                                                                                                                                                   VLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHI PVIMSL
  EQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLV
                                                                                                    YKGDEFSLIIILPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVDFKD
                                                                                                                           241 YKGDEFSLIIILPAEGMDIBEVEKLITAQQILKWLSEMQEBEVEISLPRFKVEQKVDFKD
                  EQYLHGINKE FFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGBEFGPLTRLVLV
                                                   NAIYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMWKALLRTKYGYFSESSLNYQVLELS
                                                                    NAIYFKGDWKQKFRKEDIQLINFIKKNGSTVKIPMWKALLRTKYGYFSESSINYQVLELS
                                                                                                                                                      VLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSL
                                                                                                                                                                                                                                                                                                                                                                                                 Pancreas-derived plasminogen activator inhibitor; PAPAI; human.
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/label= Signal_peptide
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15-AUG-1997; 97US-00934011.
19-FEB-1998; 98US-00026408.
12-JUL-2001; 2001US-00902684.
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                                                                                                                                                                                                                                                                                                                                                                       protein #2.
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N-PSDB; ADO05055.
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GENTZ R I
RUBEN S N
SHI Y E.
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which comprises obtaining a first soft tissue sample from an individual determining the expression of a gene in both samples and comparing the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sample indicates the presence of soft tissue sample indicates the cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The mucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                                                       99.2%; Score 1972; DB 8; Length 405;
.larity 99.5%; Pred. No. 1.3e-168;
Conservative 0; Mismatches 2; Indels (
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98JP-00044312
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Best Local Similarity
Matches 390; Conserv
                                                                                                                                                                                                                                       Sequence 405 AA;
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10-FEB-1998;
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The present sequence is encoded by a human pancpin gene. The pancpin gene encodes a protein homologous to the serine protease inhibitor of earpin. The products may be used for gene therapy, e.g. in treatment of cancers. The pancpin gene can be formulated into a drug composition for gene therapy of pancreatic cancer/tumour and for inhibition of its metastasis con suppress further malignant transformation and proliferation. Such genes can also be applied in clarifying, diagnosing, preventing and treating pancreatic cancer and its metastasis
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           Okamoto
                                                                                                                      its metastasis
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                                                                                                                                                                                                                                                                                                                                                        Length 405;
           Kyushiki H,
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                                                                                                   Drug compositions, useful for, e.g. gene therapy treatment of pancreatic cancer and inhibition of
                                                                                                                                                                                                                                                                                                                                                        Score 1968; DB 2;
Pred. No. 3.1e-168;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
             Hirano
                                                                                                                                                     Claim 1; Page 98-100; 112pp; Japanese
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             Fujiwara T,
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                                                          1999-205189/17.
              Nagata M,
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                                                                                                                                                                                                                                                                                                                               Sequence 405 AA;
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This represents a brain-associated inhibitor of tissue plasminogen activator (BAIT) polypeptide. BAIT is a member of the serpin superfamily, expressed mainly in brain tissue and probably the human analogue of chicken neuroserpin. It inhibits tissue plasminogen activator (tPA) selectively, with little effect on trypsin, thrombin or urokinase. The BAIT agens is located at chromosome 4431.2-31.3 in humans. BAIT is a regulator (inhibitor) of serine proteases and may be involved in disorders related to haemostasis, angiogenesis, tumour metastasis, cellular migration, ovulation and neurogenesis, it is used to identify collular migration, ovulation and neurogenesis. It is used to identify collular migration, ovulation and neurogenesis. It is used to identify cases where endogenous BAIT activity is insufficient, e.g. amyotrophic lateral sclerosis, motor neuron damage caused by spinal cord injury, and lateral sclerosis, motor neuron damage caused by spinal cord injury, and lateral sclerosis, motor neuron damage caused to modulate tPA where this is being used as a thrombolytic agent or where it is expressed from neural tumours. Since altered levels of BAIT are associated with some diseases to the BAIT gene can be used diagnostically to deepet impaired learning and neuron is an early including in cases of Alzhainer's disease. Other uses of BAIT and contrained and peripheral nervous systems, monitoring expression of memory, including in cases of Alzhainer's disease. Governorment of the contrainer of the matter of t
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Brain-associated inhibitor of tissue plasminogen activator; BAIT; tPA;
treatment; diagnosis; neurological disease; serpin; Alzheimer's disease;
tissue plasminogen activator; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides are as molecular weight markers, for generating antibodies and in yeast two-hybrid assays to capture specific binding proteins. Antibodies that bind apecifically to BAIT or its fragments are useful as immunoassay and in vivo imaging agents, and also for polypeptide purification. The BAIT encoding nucleic acid and probes and primers derived from it are used for gene mapping, for detecting BAIT gene expression and for isolation of related and variant genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding brain associated inhibitor of tissue plasminogen activator - and related vectors, transformed cells, poly:peptide(s), antibodies and inhibitors, useful for treating and diagnosing neurological disease and modulating activity of plasminogen
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Pred. No. 2.3e-62;
7; Mismatches 135;
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                                                                                                                                                                                        /note= "signal peptide'
                                                                                                                                                                                                                                       /note= "mature protein"
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 1A-B; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-1996;
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                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                     23-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor that is expressed specifically in the pancreas. It is the product of a cDMA clone (AAT42978) obtd. from a human pancreas library. Recombinant PDS can be produced in transformed host cells. The host cells or isolated PDS can be used to screen for opds. that modulate PDS or isolated PDS can be used as a specific protease inhibitor to treat viral infections, endotoxin or exotoxin poisoning, isohaemia, anoxia, direct trauma and other physiological or pathologoical conditions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDTIFVWSLLLLFWGSQASRCSAQKNTEFGVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                               useful in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                  is a novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1823.5; DB 2;
Pred. No. 3.1e-155;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                (AAW06202)
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                                                                                                                                                                                                                                                                                                               encoding pancreas derived serpin - pancreatic inflammation and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human pancreas-derived serpin (PDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 24-26; 36pp; English.
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                                                           96WO-US006137
                                                                                                     95US-00434881
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                                                                                                                                                 PHARM INC
                                                                                                                                                                                           Wilde CG,
                                                                                                                                                                                                                                            WPI; 1996-518311/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 366; Conserv
                                                                                                                                                                                                                                                                  N-PSDB; AAT42978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 406 AA;
                                                                                                                                                 (INCY-) INCYTE
                                                           01-MAY-1996;
                                                                                                     32-MAY-1995;
            07-NOV-1996
                                                                                                                                                                                                Braxton SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
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hemographage, by exerting a protecting effect; to prevent cell death of cells of the nervous system (claimed); to treat tissue damage in transmustantic brain injury; to treat neurodegenerative or neuroliflammatory diseases such as multiple sclerosis, to reduce the effects of epilepsy on brain tissue; to rescue endangered neurons e.g. in epileptic sclerosis and cancerous neoformations; for axonal regeneration and/or restoration of synaptic integrity and function; to prevent or cure retinal degeneration or neoanglogenesis; to regenerate injured, damaged, underdeveloped or maldeveloped brain tissue and/or nervous tissue; to treat pain; to treat psychiatric disorders such as schizophrenia; to treat pain; to treat psychiatric disorders such as schizophrenia; to treat tumors, including the prevention or reduction of the growth, expansion, infiltration and the preventions of trimmary and metasteric tumors, especially brain tumours or tumours of the retina (claimed); and to ameliorate learning and memory functions and hence raise antibodies, and in the creation of transgenic antigens and hence raise antibodies, and in the creation of transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 FKGNWKSQFRPENTRIFSFIKDDESEVQIPMMYQQGEFYYGEFSDGSNEAGGIYQVLEIP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMMKKYFNAAVNHVDFSQNVAVANYINKWVENNTNNLVKDLVSPRDFDAATYLALINAVY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 YEGDEISMMLVISRQEVPLATIEPLVKAQLVEEWANSVKKQKVEVYLPRFTVEQEIDLKD 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 VLYSLNITEIPSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LFSLLVLQSMATGATFPEEAIADLSVNMYNRLRATGEDENILFSPLSIALAMGMMELGAQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain-associated inhibitor of tissue-type plasminogen activator; BAIT; serpin; serine protease inhibitor; brain; human; Alzheimer's disease; peripheral neuropathy, multiple sclerosis; memory impairment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 HGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKGDEFSLIIILPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVDFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKD-NIIFSPLGITLVLEMVQLGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKGDWKOKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVLELS
  infarction and ischaemia, intracerebral haemorrhage and subarrachnoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.8%; Score 791.5; DB 2; 39.5%; Pred. No. 2.3e-62; ive 97; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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/label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY67239 standard; protein; 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 39.5
155, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 410 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S:
Matches 155,
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Peptide
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GSTQKEIRHSMGYDSLKNGEEFSFLKEFSNMVTAKESQYVMKIANSLFVQNGFHVNEEFL 125
                                                  184
                                                                                                    185
                                                                                                                                                 FKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVLELS 240
                                                                                                                                                                              241 YKGDEFSLIIILPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVDFKD 300
                                                                                                                                                                                                                                                                                                                                                    301 VLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSL 360
                                                                                                                                                                                                                                                                                                                                                                                 Neuroserpin, human, nervous system disorder, stroke, tumour, metastasis, retina, brain, diagnosis, therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating central nervous system disorders
                                                  HGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIY
                                                                                                 OMMKKY FINAAVNHVDFSQNVAVANY INKWVENNTNNL VKDLVS PRDFDAATYLALINAVY
                                                                                                                                                                                                                                                                                  Osterwalder T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AOSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="mature protein"
327, 360
/note= "reactive site loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krueger SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY31663 standard; protein; 410 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schrimpf SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-IB000248
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or brain or retinal tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SOND/) SONDEREGGER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-518451/43.
N-PSDB; AAX87830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human neuroserpin.
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Stoeckli ET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9941381-A1
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Gaps

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Length 410; Indels 240

19. .410 /label= BAIT

97US-00948997 96US-0028117P

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Lawrence DA, Dillon PJ, Hastings GA,
                                (HUMA-) HUMAN GENOME SCI.
(AMNA-) AMERICAN NAT RED CROSS.
                                               WPI; 2000-096374/08.
                    10-OCT-1997;
                          11-OCT-1996;
        JS6008020-A
Protein
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Coleman TA;

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This is the human brain-associated inhibitor of tissue-type plasminogen activator (BAIT) amino acid sequence. BAIT is a member of the serine protease inhibitor (serpin) family of proteins, and is widely distributed throughout the brain, but is primarily located in the neurons. A recombinant vector containing the BAIT nucleotide sequence can be used to produce a host cell that produces BAIT polypeptide. The BAIT protein selectively inhibits tissue-type plasminogen activator. The BAIT protein polymucleotides and polypeptides are useful in the diagnosis of various nervous system-related disorders in mammals which include impaired processes of learning and memory. The impaired special, olfactory and taste aversion learning, learning and memory impairments associated with Alzheimer's disease can be diagnosed using the BAIT sequences. BAIT polypeptides and agonists are used for treating an individual in need of an increased level of BAIT activity. BAIT agonists are also useful for treating Alzheimer's disease and peripheral neuropathies such as multiple celerosis. Motor neuron or sensory neuron damage resulting from spinal cord injury may also be prevented or treated with BAIT agonists. BAIT activity an individual in need of a decreased
                                                                                                     New nucleic acid encoding human brain-associated inhibitor of tissue-type plasminogen activator, useful in the diagnosis of various nervous system-related disorders in mammals.
                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 48pp; English
N-PSDB; AAZ56164
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                                                                        6 LWSLLLLFFGSQASRCSAQXNTEFAVDLYQEVSLSHKD-NIIFSPLGITLVLEMVQLGAK 64
                                                                                                65 GKAQQQIRQTLKQQETSAGBEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYL
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Length 410;
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39.8%; Score 791.5; DB 3; 39.5%; Pred. No. 2.3e-62; tive 97; Mismatches 135;
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 Query Match
Best Local Similarity 39.5%
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306 VLKALGITEIFIKDANLTGLSDNKEIFLSKAIHKSFLEVNEEGSEAAAVSGMIAISRMAV 365 366 LYPQVIVDHPFFFLIRNRRTGTILFMGRVMHP 397 유 ò d

completed: October 21, 2004, 06:42:08 ne : 72 secs Job time : Search

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Sequence 2, Appli
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Sequence 88, Appl
Sequence 67, Appl
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1: /cgn2 6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-628-395-2

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US-09-95-485-2

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US-10-355-208-2

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US-10-752-041-3
US-10-023-634-88
US-10-037-417-67
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Maximum DB seg length: 200000000
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-60-SD	US-10-	US-10-	-08-7	-60-SD	US-09-	US-10-0	US-10-	US-10-	US-10-	-60-SN	US-10-	US-10-	US-10-	US-10-	US-10-	-60-SD	US-10-	-60-SD	US-10-	US-10-	US-10-	US-10-	US-10-	6-60-	US-10	US-10-	US-10-	US-10	US-10-	ns
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## ALIGNMENTS

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RESULT 1

10S-09-902-684-2

10S-09-902-684-2

Sequence 2, Application US/09902684

Patent No. USZ0020127640a1

GENERAL INFORMATION:

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TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEM ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOX P.L.L.C.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1987; DB 15;
100.0%; Pred. No. 6.5e-156;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN &
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
FILING DATE: 16-AUG-1996
ATTORNEY/AGBNI TUPORMATION:
NAME: STREFE, ERLC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0300002
TELECOMMINICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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APPLICATION NUMBER: US/09/902,684
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                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09902684 Patent No. US20020127640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                        LENGTH: 392 amino acids TYPE: amino acid
                                                                                                                                                       TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 392; Conservative
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APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
INHIBITOR
                                                                                                                                                                                                        Length 392;
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UDMER: US/10/628,395
FILING DATE: 29-Jul-2003
CLASSIFICATION: <UNknown>
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100.0%; Pred. No. 6.5e-156;
ive 0; Mismatches 0;
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FILING DATE: 19-FEB-2001
FILING DATE: 15-AUG.
FILING DATE: 15-AUG.
APPLICATION NUMBER: US 60/024,055
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ADDRESSEE: STERNE, KESELER, GO
STREET: 1100 NEW YORK AVENUE,
CITY: WASHINGTON
STATE: DC
                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10628395; Publication No. US20040086978A1; GENERAL INFORMATION: APPLICANT: Ni et al.
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    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 392; Conservative
                                                                                                                                                            US-09-902-684-2
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LGAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVK 120
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Parent No. US20020143165A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
TITLE OF INVENTION: Activator
FILE REFERENCE: PF336P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLV
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                                               Version #1.30
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1488.0300002
TELECOMMUNICATION INFORMATION:
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                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: 19-FEB-2001
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1966
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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    COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/628,395
FILING DATE: 29-Jul-2003
CLASSIFICATION: 《Unknown》
                                                                                                                                                                                                                                                                                                              NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
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Best Local Similarity 100.
Matches 392; Conservative
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US-10-628-395-13
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US-09-957-485-2
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TITLE OF INVENTION: PANCREAS-DERIVED PLASMINGEN ACTIVATOR
INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1987; DB 9; Best Local Similarity 100.0%; Pred. No. 6.8e-156; Matches 392; Conservative 0; Mismatches 0;
                                                                  FILING DATE: «Unknown)
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY AGRNT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0300002
TELEPHONE: 202-371-2500
TELEPHONE: 202-371-2540
INFORMATION POR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-902-684-13
            CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,408
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FILING DATE: 12-Jul-2001
                                                                                                                                                                                                                                                                                                                       LENGTH: 405 amino acids TYPE: amino acid
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COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
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US-10-628-395-13
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Sequence 2, Application US/10355208
Publication No. US20040038880A1
GENERAL INFORMATION:
APPLICATION NO. US20040038880A1
GENERAL INFORMATION:
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE REFERENCE: PF135F1
CURRENT APPLICATION NUMBER: US/10/355,208
CURRENT APPLICATION NUMBER: US/09/521,664
PRIOR APPLICATION NUMBER: US/09/521,664
PRIOR APPLICATION NUMBER: US/09/521,664
PRIOR APPLICATION NUMBER: US/09/521,664
PRIOR PLING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                   65 GKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 GSTQXEIRHSMGYDSLKNGBEFSFLKEFSNMVTAKESQYVMKIANSLFVQNGFHVNBEFL 125
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                                                                                                                                                                                                                   Length 410;
                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                             39.8%; Score 791.5; DB 9;
llarity 39.5%; Pred. No. 5.8e-57;
Conservative 97; Mismatches 135;
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  NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver.
SEQ ID NO 2
                                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-09-987-021-2
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ORGANISM: Homo sapiens
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155; Conserv
                                                                                 LENGTH: 410
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Best Local S
Matches 155
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Sequence 2, Application US/09987021

Sequence 2, Application US/09987021

Sequence 2, Application US/09987021

Sequence 2, Application US/09020165147A1

APPLICANT: Yepes, et al.

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator

FILE REFERENCE: F83667

CURRENT APPLICATION NUMBER: US/09/987,021

CURRENT FILING DATE: 2001-09-21

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-11-4

PRIOR APPLICATION NUMBER: 09/221,664

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-01
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                  CURRENT FILING DATE: 2001-09-73

PRIOR APPLICATION NUMBER: US 09/521,664

PRIOR FILING DATE: 2000-03-08

PRIOR PLING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 2
CURRENT APPLICATION NUMBER: US/09/957,485
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                              LENGTH: 410
                                                                                                                                                                                                                                                                                      ; ORGANISM: no
US-09-957-485-2
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TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
TITLE OF INVENTION: Activator
FILE REFERENCE: PF336P1
CURRENT APPLICATION NUMBER: US/09/957,485
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 09/521,664
PRIOR PILING DATE: 1999-03-10
PRIOR PILING DATE: 1999-03-10
SROFTWARE: Patentin Ver. 2.1
SSOFTWARE: Patentin Ver. 2.1
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                                                                                                                                   241 YKGDEFSLIIILPAEGMDIEBVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVDFKD
HGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIY
                           QMMKKYFNAAVNHVDFSQNVAVANYINKWVENNTNNLVKDLVSPRDFDAATYLALINAVY
                                                                 FKGDWKQKFRKEDTQLINFTKKNGSTVKIPWMKALLRTKYGYFSESSLN----YQVLELS
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Best Local Similarity 40.0%
Matches 158; Conservative
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CRGANISM: Gallus gallus
US-09-957-485-3
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US-09-957-485-3
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TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator
CURRENT PILIS DATE: 2004-01-07
PRIOR PILING DATE: 2003-01-11
PRIOR PILING DATE: 2001-11-13
PRIOR PELICATION NUMBER: 09/957,485
PRIOR PELING DATE: 2000-11-13
PRIOR PELING DATE: 2000-11-14
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-01-01
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     66 GSTQKEIRHSMGYDSLKNGEEFSFLKEFSNMVTAKESQYVMKIANSLFVQNGFHVNEEFL 125
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                                                                     QMMKKY FINAAVNHVDFSQINVAVANY INKWVENNTINIL VKDLVSPRDFDAATYLALINAVY
                                                                                                        FKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVLELS
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Pred. No. 5.8e-57;
7; Mismatches 135;
                                                                                                                                                                                                                                                                                                                    361 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10752041 Publication No. US20040203101A1 GENERAL INFORMATION:
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Similarity 39.5%;
55; Conservative 97
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SEQ ID NO 2
LENGTH: 410
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US-10-752-041-2
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Best Local Simi
Matches 155;
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US-10-752-041-2
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APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE OF INVENT APPLICATION NUMBER: US/10/355,208
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US/09/521,664
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-10
NUMBER OF SEC ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Hastings, et al.

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE OF INVENTION NUMBER: US/10/752,041

CURRENT APPLICATION NUMBER: US/10/752,041

PRIOR APPLICATION NUMBER: US/3021

PRIOR APPLICATION NUMBER: 09/997,021

PRIOR APPLICATION NUMBER: 09/997,021

PRIOR APPLICATION NUMBER: 09/997,485

PRIOR APPLICATION NUMBER: 09/957,485

PRIOR APPLICATION NUMBER: 09/927,485

PRIOR APPLICATION NUMBER: 09/122,292

PRIOR PLING DATE: 2000-11-28

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 2000-11-14
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Pred. No. 1e-56;
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    Sequence 3, Application US/10355208
Publication No. US20040038880A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10752041 Publication No. US20040203101A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 40.09
158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Gallus gallus
US-10-355-208-3
                                                                                                                                                                                                                                                                                                                                             410
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Best Local S:
Matches 158
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                                                                                                                                                                                              APPLICANT: Yepes, et al TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE REFERENCE: PF336P2 FORMER: US/09/987,021 CURRENT APPLICATION NUMBER: US/09/987,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 FLWSLLLLFFGSQASRCSAQKNT--EFAVDLYQEVSLSHKD-NIIFSPLGITLVLEMVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 788.5; DB 9; Length ; Pred. No. 1e-56; 92; Mismatches 138; Indels
|::||||||:|| 363 MAVLYPQVIVDHPFFFLVRNRRTGTVLFMGRVMHP 397
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                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/97, 485
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/24,971
PRIOR APPLICATION NUMBER: 09/21,664
PRIOR APPLICATION NUMBER: 09/348,817
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 09/348,817
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 08/948,97
PRIOR PRILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 08/948,97
PRIOR PRILING DATE: 1997-10-10
PRIOR PRILING DATE: 1997-10-10
PRIOR PLING DATE: 1996-10-11
NUMBER: 0F SEQ ID NOS: 18
                                                                                                                                   Sequence 3, Application US/09987021
Patent No. US20020165147A1
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40.0%;
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Best Local Similarity 40.09
Matches 158; Conservative
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ORGANISM: Gallus gallus
                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-987-021-3
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SEQ ID NO 3
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RESULT 11 US-10-355-208-3

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APPLICANT: Malyankar, Uriel M
APPLICANT: Gunther, Erik
APPLICANT: Gunther, Erik
APPLICANT: Saithson, Glennda
APPLICANT: Millet, Isabella
APPLICANT: Garlach, Valerie
ITILE OF INVENTION: Using the Same
ITILE OF INVENTION: Using the Same
FILE REPRENCE: 21402-221
CURRENT APPLICATION NUMBER: 06/256,163
PRIOR APPLICATION NUMBER: 06/256,163
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/276,688
PRIOR PLING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/277,880
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-04-25
PRIOR PLING DATE: 2001-08-29
PRIOR PLING DATE: 2001-08-20
PRIOR PLING DATE: 2001-08-29
PRIOR PLING DATE: 2001-08-20
PRIOR PLING DATE: 2001-08-29
PRIOR PLING DATE: 2001-08-20
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US-10-037-417-67
Sequence 67, Application US/10037417
Publication No. US20040052806A1
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US-10-023-634-88
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  PRIOR APPLICATION NUMBER: 09/521,664
PRIOR FILING DATE: 2000-03-08
PRIOR PELLING NUMBER: 09/348,817
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/123,704
PRIOR APPLICATION NUMBER: 60/023,704
PRIOR PILING DATE: 1999-03-10
PRIOR PILING DATE: 1996-10-11
PRIOR PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 3
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Publication No. US20302353891
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A
APPLICANT: SOLMAN, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Ballinger, Robert A
APPLICANT: Ballinger, Robert A
APPLICANT: Goo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Shenoy, Suresh G
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Casman, Stacie J
Boldog, Ferenc
Gusev, Vladimir Y
Burgess, Catherine E
Edinger, Shlomit R
Gangolli, Esha A
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Zerhusen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                    148 EMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKEDTQLINFTKKN 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TTŤVKVPNMSQTGRŤ-FRÝGRDEBLNCQVLBLPÝKGNA-SMLÍÍLÞDEG-GLBTVÉKALT 236
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                                                                                                                                                                  32 DLYQEVSLSHKD-NIIFSPLGITLVLEMVQLGAKGKAQQQIRQTL--KQQETSAGEEFLV 88
                                                                                                                                                                                                                                        2 DLYKELAKESPDKNIFFSPVSISSALAMLSLGAKGSTATQILEVLGFNLTETSEADIHQG 61
Query Match 35.5%; Score 706; DB 14; Length 360;
Best Local Similarity 43.3%; Pred. No. 5.8e-50;
Matches 158; Conservative 66; Mismatches 131; Indels 10; Gaps
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208 GSTVKIPMAKALLRTKYGYFSESSLNYQVLELSYKGDEFSLIIILPAEGMDIEEVEKLIT 267
                                                                                                                                              180 TTTVKVPMMSQTGRT-FRYGRDEELNCQVLELPYKGNA-SMLIILPDEG-GLETVEKALT 236
                                                                                                                                                                                                         268 AQQILKWLSEMQEEEVEISLPRFKVEQKVDFKDVLYSLNITEIFSGGCDLSGITDSSEVY 327
                                                                                                                                                                                                                                                                                                                                                           297 VSKVVHKAFLEVNEEGTEAAATGV-IIVPRSLPPPEFKANRPFLFLIRDNPTGSILFMG 355
                                                                                                                                                                                                                                                           237 PETLKKWIKSLIKRSVELYLPKFKLEISYDLKDVLEKLGIIDLFSNKADLSGISEDKDLK 296
                                                                                                                                                                                                                                                                                                                        328 VSQVTQKVFFEINEDGSBAATSTGIHIPVIMSLAQSQFIANHPFLFIMKHNPTESILFMG 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Patturajan, Meera
APPLICANT: Shamkets, Richard A
APPLICANT: Specen K
APPLICANT: Specen, Kimberly
APPLICANT: Taupier, Raymond J
FILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR PLING DATE: 2000-03-30
PRIOR PLING DATE: 2000-03-30
PRIOR PLING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR PLING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,08
PRIOR PLING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-10
PRIOR PLING DATE: 2000-04-10
PRIOR PLING DATE: 2000-04-10
PRIOR PLING DATE: 2000-04-10
PRIOR PLING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-13
PRIOR PLING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-14
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Publication No. US20030096952A1
GENERAL INFORMATION:
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APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kumud
APPLICANT: Padigaru, Muralidhar
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LENGTH: 377
TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-187-31
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43.3%; Pred. No. 5.8e-50;
tive 66; Mismatches 131; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE OF INVENTION: Proteins and Nucleic Acids Encoding Same LE REFERENCE: 21402-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR PLILING DATE: 2002-00-05
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-08
PRIOR PLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR PRIOR DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
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PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 360
                           : Kekuda, Ramesh
: Alsobrook II, John P
Tchernev, Velizar T
: Liu, Kiachong
: Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPLICANT: Taupier Jr, Raymond J
RPLICANT: Miller, Charles E
RPLICANT: Bisen, Andrew J
HILE OF INVENTION: Proteins and N
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Padigaru, Muralidhara
                                                                                                                                                                       Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
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Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
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Vernet, Corine A.M.
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Edinger, Shlomit R
Sciore, Paul
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Guo, Xiaojia
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Matches 158; Conservative
GENERAL INFORMATION:
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140 FQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIYFKGDWKQKFRKEDTQ 199
                                                        320 JTDSSEVYVSQVTQKVFFEINEDGSEAATSTGI-----HIPVIMSLAQSQFIANHPFLFI 374
                                                                                                                                                    80 TSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKEQYLHGNKEFFQSAIKLVD 139
                          9 ASANADFAFSLYKELVEQNPDKNIFFSPVSISSALAMLSLGAKGNTATQILEVLGFNLTE 68
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Search completed: October 21, 2004, 06:57:23 Job time : 132 secs

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Query Match
Best Local Similarity
Matches 392; Conserv
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Sequence 2, Appli
Sequence 13, Appl
Sequence 13, Appl
                                                                                     October 21, 2004, 06:38:56; Search time 40 Seconds (without alignments) 649.916 Million cell updates/sec
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Sequence 2,
Sequence 2,
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1987
1 MDTIFLWSLLLLFFGSQASR......FIMKHNPTESILFMGRVTNP 392
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Sequence 2,
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Sequence
Sequence
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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3. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-902-684-1
US-09-026-684-13
US-09-902-684-13
US-08-474-711-2
US-09-361-773-2
US-09-361-773-2
US-09-348-897-2
US-09-722-292-2
US-09-722-292-2
US-09-722-292-3
US-09-722-292-3
US-09-722-292-3
US-09-722-297-3
US-08-947-0828-2
US-08-947-0828-2
US-08-947-0828-4
US-08-967-040-4
US-08-266-147-8-2
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                                                                                                                                                                                                                                                        478139 seqs, 66318000 residues
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                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
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seq length: 200000000
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Match Length DB
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                                                                                                                                                   Title:
Perfect score:
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Maximum DB
                                                              OM protein
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                                                                                                                                                                                   Sequence:
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Sequence 4, Appli	Sequence 4, Appli	4		~		Sequence 8, Appli	œ	Sequence 5, Appli		nce 5	Patent No. 5457090	Patent No. 5495001	Patent No. 5457090	. 51	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli
US-08-121-714-4	US-08-477-108A-4	US-08-477-112-4	PCT-US93-08322-4	US-08-121-714-8	US-08-477-108A-8	US-08-477-112-8	PCT-US93-08322-8	US-08-948-997-5	US-09-348-817A-5	US-09-722-292-5	5457090-2	5495001-7	5457090-4	5187089-9	US-08-948-997-4	US-09-348-817A-4	US-09-722-292-4
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573.5	573.5	573.5	573.5	569.5	569.5	569.5	569.5	562.5	562.5	562.5	ഹ	562.5	19	29		558	558
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## ALIGNMENTS

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PARENT NOTE 408-05

US-09-026-408-05

Sequence 2, Application US/09026408

Patent No. 530338

GENERAL INFORMATION:
PAPLICANT: NI tet al.
TITLE OF INVENTION:
INTELE ILON NEW YORK AVENUE, SUITE 600
CITY:
ADDRESSEE: STRENE KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: LION NEW YORK AVENUE, SUITE 600
CITY:
MADINGTON OF AVENUE, SUITE 600
CITY:
MADINGTON OF AVENUE, SUITE 600
CONNTRY: US
COMMOTIVE RADAMALE PORM:
MEDIUM TYPE:
MEDIUM TYPE:
MEDIUM DATA:
PROPERATION STREET:
MAPLICATION NUMBER: US 60/024,056
FILING DATE:
FILING DAT
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Mismatches
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FELECOMMUNICATION INFORMATION:
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                                                                 100.0%;
                                                           Query Match
Best Local Similarity 100.
Matches 392; Conservative
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MDTIFLWSLLLLFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ 60
                                                 MDTIFLWSLLLIFFGSQASRCSAQKNTEFAVDLYQEVSLSHKDNIIFSPLGITLVLEMVQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09902684
Sequence 10, 649738
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NBW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,684
FILING DATE: 12-Jul-2001
CLASSIFICATION: CURNOWN>
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FILING DATE: cUnknown>
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K.
REGISTRATION NUMBER: 36,688
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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TYPE: amino acid
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US-09-902-684-2
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Length 392;
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Patent No. 630338

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF SEQUENCES:

TORRESPONDENCE: 15

CORRESPONDENCE: 15

CORRESPONDENCE: 15

CORRESPONDENCE: 16

CORRESPONDENCE: 16

CORRESPONDENCE: 16

CORRESPONDENCE: 16

CORRESPONDENCE: 16

CORRESPONDENCE: 10

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STATE: DC...
COUNTRY: USA
CONFUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN Release #1.0, Version #1.30
SOFTWARE: PatchIN DATA:
APPLICATION NUMBER: US/09/026,408
FILLING DATE: Herewith
Score 1987; DB 4;
Pred. No. 1.1e-187;
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Pred. No. 1.2e-187;
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Patent No. S804376
GENERAL INFORMATION:
APPLICANT: Braxton, Scott M. APPLICANT: Wilde, Craig G. APPLICANT: Diep, Dinh TITLE OF INVENTION: Pancreas-Derived Serpin NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
STREET: 3330 Hillview Avenue
              REFERENCE/DOCKET NUMBER: 1488.0300002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                      INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHRRACTERISTICS:

TYPE: amino acids

TYPE: amino acids

DODOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-902-684-13
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CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/434,881
FILING DATE: Herewith
CLASSIFICATION: 435
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 392; Conservative
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US-08-434-881-2
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                                                                                                                                                                                             Gaps
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Sequence 13, Application US/09902684
Patent No. 6649738
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR INHIBITOR
                                                                                                                                                         DB 3; Length 405;
                                                                                                                                                                                           Indels
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                                                                                                                                                                                               ..
                                                                                                                                                         100.0%; Score 1987; DB 3;
100.0%; Pred. No. 1.2e-187
iive 0; Mismatches 0;
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ADDRESSE: STERNE, KESCLER, GOLDSTE:
STREET: 1100 NEW YORK AVENUE, SUITE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/026,408
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/902,684
FILING DATE: 12-Jul-2001
CLASS:FICATION: <Unknown>
PRIOR APPLICATION DATA:
        13:
    INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 405 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCES:
                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 392; Conservative
                                                                                                   ; MOLECULE TYPE: protein US-09-026-408-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-902-684-13
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61 LGAKGRAQQXXRQTLQQQEXSAGEEFLCXEVIFSLPSQRRWK---NLHLILDPMPSTXQEG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                           89.5%; Score 1777.5; DB 3; 90.4%; Pred. No. 5.9e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 IMSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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Patent No. 6197519
GENERAL INFORMATION:
APPLICANT: Braxton, Scott M.
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Pancreas-Derived Serpin
NUMBER OF SEQUENCES: 2
COMPRESPONDENCE ADDRESS:
ADDRESSED: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3330 Hillview Avenue CITY: Palo Alto STATE: California
                                                                                                                                                              S
                                                                                                                                                              PF0035
                                                08/ 434,881
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther. Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PFOG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-0195
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 entine acids
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                           PRIOR APPLICATION DATA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 358; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                Score 1777.5; DB 1; Length 406;
Pred. No. 5.9e-167;
7; Mismatches 24; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STREET: 3330 Hillview Avenue
CITY: Palo Alto
STATE: California
CONNTRY: USA
ZIP: 94304
CONNTRY: USA
ZIP: 94304
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/08/977.771
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 IMSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Diep, Dinh
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3330 Hillview Avenue
                                                                   PF0035 US
                  NAME: Luther, Barbara J.
REGISTATION NUMBER: 395PG;
REFERENCE/DOCKET NUMBER: PFOT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0155
TELEPAX: 415-85-0155
TELEPAX: 415-85-015
SEQUENCE CHARATERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08977771
Patent No. 6013448
                                                                                                                                                                                                                                                                                                                            Query Match 89.5%;
Best Local Similarity 90.4%;
Matches 358; Conservative
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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186 FKGNWKSQFRPENTRTFSFTKDDESEVOIPWMYQQGEFYYGEFSDGSNEAGGIYOVLEIP 245
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Batent No. 6191260
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENITON: Brain-Associated Inhibitor of Tissue-Type Plasminogen
TITLE OF INVENITON: Activator
FILE PEFERRNCE: PF3361
CURRENT APPLICATION NUMBER: US/09/348,817A
CURRENT APPLICATION NUMBER: 08/948,997
PRIOR APPLICATION NUMBER: 08/948,997
PRIOR FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LESLLVLOSMATGATFPERALADLSVNNYNRLRATGEDENILFSPLSIALAMGMMELGAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 HGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVLELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 410;
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                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 791.5; DB 3;
Pred. No. 1.4e-69;
7; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYPOVIVDHPFFFLIRNRRIGTILFMGRVMHP 397
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                                                                                                                                                     SOFTWARE: FALLELLING CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,997
FILING DATE: Oct.10-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTALION NUMBER: 9F336
REGISTALION NUMBER: PF336
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8514
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TELEPHONE: (301) 309-8514
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TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8515
SEQUENCY: (301) 309-8516
                ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.8%; Score
39.5%; Pred
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Best Local Similarity 39.5%
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-948-997-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 FTVKEQYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLIR 176
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APPLICANT: COLEMAN, TIM
APPLICANT: COLEMAN, TIM
TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1777.5; DB 3;
Pred. No. 5.9e-167;
7; Mismatches 24;
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            CURRENT ARE: Factorial Dark:
APPLICATION DATA:
APPLICATION NUMBER: US/09/361,773
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/977,771
FILING DATE:
APPLICATION NUMBER: 08/977,771
FILING DATE:
APPLICATION NUMBER: 08/977,771
FILING DATE:
APPLICATION NUMBER: 08/977,771
FILING DATE:
APPLICATION NUMBER: 08/939.54
REFERENCE', Barbara J.
NAME: Luther, Barbara J.
RECISTRATION UNBER: 33954
REFERENCE', DOCKET NUMBER: PF0035 US
TELECONMUNICATION INFORMATION:
TELECONMUNICATION INFORMATION:
TELECONMUNICATION SEQ ID NO: 2:
SUBJUNCE CHARACTERISTICS:
FENDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-948-997-2; Sequence 2, Application US/08948997; Sequence No. 6008020; General Information:
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Best Local Similarity
Matches 358; Conserv
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Gaps .. ..

Length 410;

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126 OMMKKYFNAAVNHVDFSQNVAVANYINKWVENNTNNLVKDLVSPRDFDAATYLALINAVY 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hastings et al.

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
TITLE OF INVENTION: Activator
FILE REFERENCE: PF336D1
                                                                                                                                                                                                                                                                                                                                                                        66 GSTQKEIRHSMGYDSLKNGEEFSFLKEFSNWVTAKESQYVMKIANSLFVQNGFHVNEEFL
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                                                                                                                                                                Score 791.5; DB 4; Length
Pred. No. 1.4e-69;
97; Mismatches 135; Indels
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39.7%; Score 788.5; DB 3;
Best Local Similarity 40.0%; Pred. No. 2.8e-69;
Matches 158; Conservative 92; Mismatches 138;
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CURRENT FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 08/948,997
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/028,117
PRIOR FILING DATE: 1996-10-11
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; Sequence 3, Application US/09348817A
; Patent No. 6191260
                                                                                                                                                                39.8%;
ilarity 39.5%;
Conservative 9
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  ; LOCATION: (1)...(410)
; NAME/KEY: signal
; LOCATION: (1)...(18)
; NAME/KEY: chain
; LOCATION: (19)...(410)
US-09-722-292-2
                                                                                                                                                             Query Match
Best Local Similarity
Matches 155; Conserva
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SEQ ID NO 3
LENGTH: 410
TYPE: PRT
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US-09-348-817A-3
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Sequence 2, Application US/0972292

Fatent No. 6541452

GENERAL INFORMATION:

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen

TITLE OF INVENTION: Activator

TITLE OF INVENTION NUMBER: US/09/722,292

CURRENT APPLICATION NUMBER: US/09/348,817

PRIOR APPLICATION NUMBER: 60/028,117

PRIOR APPLICATION NUMBER: 60/028,117

PRIOR FILING DATE: 1995-07-08

PRIOR FILING DATE: 1995-10-11

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1
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PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 2
LENGTH: 410
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Best Local Similarity 39.59
Matches 155; Conservative
                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: chain
LOCATION: (19)...(410)
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LOCATION: (1)..(410)
NAME/KEY: signal
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NAME/KEY: Propep
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US-09-348-817A-2
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US-09-722-292-2
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Query Match
Best Local Simi:
Matches 154;
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US-08-948-997-3
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Sequence 3, Application US/0972292;
Sequence 3, Application US/0972292;
Sequence 3, Application US/0972292;
GENERAL INFORMATION:
APPLICANT: Hastings et al.
TITLE OF INVENTION: Activator
TITLE OF INVENTION: Activator
FILE REPERENCE: FF336D1
CURRENT APPLICATION NUMBER: US/09/722,292
CURRENT FILING DATE: 2000-11-28
PRIOR FPLING DATE: 1999-07-08
PRIOR FILING DATE: 1996-10-11
SPRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFLQLVKKYFKAEVENIDFSQSAAVATHINKAVENHTNNMIKDFVSSRDFSALTHLVLIN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIYFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSYKGDEFSLIILLPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKDVLYSLNITELFSGGCDLSGITDSSEVYVSQVTQKVFPEINEDGSEAATSTGIHIPVI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVN 181
                                                                                                                                   AIYFKGNWKSQFRPENTRIFSFIKDDETEVQIPMMYQQGBFYYGBFSDGSNBAGGIYQVL 242
                                                                                                                                                                                                        243 BIPYEGDEISMAIVLSRQEVPLVTLEFLVKASLINEWANSVKKQKVEVYLPRFTVEQEID 302
                                                                                                                                                                                                                                                                                  182 AIYFKGDWKQKFRKEDIQLINFIKKNGSIVKIPMMKALLRIKYGYFSESSLN----YQVL 237
                                                                                                                                                                                  ELSYKGDEFSLIIILPAEGMDIEEVEKLITAQQILKWLSEMQEEEVEISLPRFKVEQKVD 297
                                                                                                                                                                                                                                                         FKDVLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVI 357
GAHGTTLKEIRHSLGFDSLKNGEBFTFLKDLSDMATTEESHYVLNMANSLYVQNGFHVSE 122
                                     QYLHGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGFLTRLVLVN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 FLGLLSLLVLPSKAFKTNFPDETIAELSVNVYNQLRAAREDENILFCPLSIAIAMGMIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GAKGKAQQQIRQTLKQQETSAGEEFLVLKSFCSAISEKKQEFTFNLANALYLQEGFTVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 FLWSLLLLFFGSQASRCSAQXNT--EFAVDLYQEVSLSHKD-NIIFSPLGITLVLEMVQL
                                                        7;
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39.7%; Score 788.5; DB 4;
Best Local Similarity 40.0%; Pred. No. 2.8e-69;
Matches 158; Conservative 92; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                       363 MAVLYPQVIVDHPFFFLVRNRRTGTVLFMGRVMHP 397
                                                                                                                                                                                                                                                                                                                                   358 MSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-722-292-3
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US-09-722-292-3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 FLWSLILLIFFGSQASRCSAQKNTEFAV-DLYQEVSLSHKDNIIFSPLGITLVLEMVQLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 YFKGDWKQKFRKEDTQLINFTKKNGSTVKIPMMKALLRTKYGYFSESSLN----YQVLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                               Sequence 3, Application US/08948997
; Sequence 3, Application US/08948997
; Patent No. 6008020
; GENERAL INFORMATION:
    APPLICANT: HASTING, GREGG
    APPLICANT: LAWRENCE, DANIEL
    TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
    TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
    ADDRESSE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.0%; Score 756; DB 3; Length 40 ilarity 39.2%; Pred. No. 4.4e-66; Conservative 90; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/948,997 FILING DATE: OCC-10-97
                      363 MAVLYPOVIVDHPFFFLVRNRRTGTVLFMGRVMHP 397
358 MSLAQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                                                                       E: HUMAN GENOME SCIENCES, INC
9410 KEY WEST AVENUE
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3R: PF336
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NAME: A. ANDERS BROOKES
REGIGSTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 407 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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241 YKGDEFSLIIILPARGMDIBEVEKLITAQQILKWLSEMQEBEVEISLPRFKVEQKVDFKD 300
                                                                                                  246 YEGDEISMMLVLSRQEVPLATLEPLVKAQLVEEWANSVKKQKVEVYLPRFTVEQEIDLKD 305
                                                                                                                                               301 VLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMSL 360
                                                                                                                                                                            306 VLKALGITEIFI-KIKFDSLSDNKEIFLSKAIHKSFLEVNEEGSELSVS-GM-IQLVGCC 362
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                                                                                                                                                                                                                                  361 AQSOFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                            363 LYPQVIVDHPFFFLIRNRRTGTILFMGRVMHP 394
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3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,040
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08997040
Patent No. 5929210
GENERAL INFORMATION:
APPLICANT: Baxton, Scott M.
APPLICANT: Stuart, Susan G.
TITLE OF INVENTION: NOVEL SERPIN DEI
TITLE OF INVENTION: HYPOTHALAMUS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,823
FILING DATE: 07-JUN-1995
ATTONEY/DRAPY LORRATION:
NAMB: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Diskette
IBM Compatible
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amino acid
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Diskett
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STATE: C.
COUNTRY:
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US-08-997-040-2
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DVLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHIPVIMS 359
                          6 GSTQKEIRHSMGYDSLKNGEEFSFLKEFSNMVTAKESQYVMKIANSLFVQNGFHVNEEFL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.8%; Score 751; DB 1; Length 407; Best Local Similarity 38.8%; Pred. No. 1.4e-65; Matches 152; Conservative 95; Mismatches 137; Indels
                                                                                                                                                                                                                     Sequence 2, Application US/08487823B
Patent No. 5700924
GENERAL INFORMATION:
APPLICANT: Braxton, Scott M.
APPLICANT: Diep, Dinh
APPLICANT: Brust, Susan G.
TITLE OF INVENTION: HYPOTHALAMUS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                          362 VLYPQVIVDHPFFFLVRNRRTGTVLFMGRVMHP 394
                                                                              360 LAQSQFIANHPFLFIMKHNPTESILFMGRVTNP 392
                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Drive Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,823B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATONNEY, AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0039 US
FELECHMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-852-0195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Diskette
IBM Compatible
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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  300
                                       302
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STATE:
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126 OMMKKYFNAAVNHVDFSQNVAVANYINKWVENNTNNLVKDLVSPRDFXAATYLALINAVY 185
                                                                                             185 FKGDWKOKFRKEDTQLINFTKKNGSTVKIPMMKALLRIKYGYFSESSLN----YQVLELS 240
                                                                                                                 186 FKGNWKSQFRPENTRIFSFTKDDBSEVQIPMMYQQGEFYYGEFSDGSNEAGGIYQVLEIP 245
                                                                                                                                                                                                                            301 VLYSLNITEIFSGGCDLSGITDSSEVYVSQVTQKVFFEINEDGSEAATSTGIHLPVIMSL 360
                                                                                                                                                                                                                                             66 GSTQKEIRHSMGYDSLKNGEEFSFLKEFSNMVTAKESQYVMKIANSLFVQNGFHVNEEFL 125
                               125 HGNKEFFQSAIKLVDFQDAKACAEMISTWVERKTDGKIKDMFSGEEFGPLTRLVLVNAIY 184
                                                                                                                                                                                                                                                                                          361 AOSOFIANHPFLFIMKHNPTESILFMGRVTNP 392
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